

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:16:02 ; Search time 62.7613 Seconds
(without alignments)
1359.585 Million cell updates/sec

Title: PCT-US03-05147-3
Perfect score: 1643
Sequence: 1 METDTLLLVWLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1643	100.0	302	4	AAB60699	Aab60699 Mouse IgG
2	1643	100.0	302	4	AAE00507	Aae00507 Human BCM
3	1488.5	90.6	283	5	AAE15488	Aae15488 Human BCM
4	1398.5	85.1	281	5	AAE15489	Aae15489 Mouse BCM
5	1379	83.9	334	5	AAO14133	Aao14133 Protein o
6	1376	83.7	366	5	AAO14132	Aao14132 Protein o
7	1361	82.8	320	5	AAE22245	Aae22245 Murine Ig
8	1361	82.8	320	6	ABR55865	Abr55865 Human imm
9	1271	77.4	332	6	AAE35228	Aae35228 Human TAC

10	1269	77.2	446	4	AAE13055	Aae13055	ADAM-17di
11	1268.5	77.2	633	3	AAy84965	Aay84965	Amino aci
12	1265.5	77.0	465	4	AAE13053	Aae13053	ADAM-10di
13	1264.5	77.0	404	5	AAO14136	Aao14136	Protein o
14	1263	76.9	348	6	AAE35225	Aae35225	Human TAC
15	1260	76.7	608	6	ABJ37102	Abj37102	Concatame
16	1259.5	76.7	397	5	AAE15498	Aae15498	Human TAC
17	1259	76.6	480	6	AAO16239	Aao16239	B7-relate
18	1259	76.6	480	6	AAO16238	Aao16238	B7-relate
19	1259	76.6	698	5	AAU81012	Aau81012	B7-relate
20	1259	76.6	698	6	AAO16237	Aao16237	B7-relate
21	1258	76.6	344	6	AAE35224	Aae35224	Human TAC
22	1257.5	76.5	376	2	AAW60037	Aaw60037	Antigenic
23	1256	76.4	422	4	AAB66993	Aab66993	OPG-Fc. 4
24	1254	76.3	266	5	ABB77128	Abb77128	Human Cri
25	1254	76.3	266	5	ABB77121	Abb77121	Human Cri
26	1254	76.3	494	4	AAE13051	Aae13051	ADAM-8dis
27	1253.5	76.3	357	6	AAE35226	Aae35226	Human TAC
28	1252	76.2	266	5	ABB77108	Abb77108	Human Cri
29	1252	76.2	266	5	ABB77115	Abb77115	Human Cri
30	1252	76.2	444	6	ABJ37098	Abj37098	Concatame
31	1252	76.2	628	6	ABJ37100	Abj37100	Concatame
32	1251.5	76.2	523	4	AAE13057	Aae13057	ADAM-21di
33	1251	76.1	400	4	AAB80901	Aab80901	Human OPG
34	1251	76.1	400	4	AAy72919	Aay72919	Human OPG
35	1251	76.1	445	2	AAy24153	Aay24153	Bovine LO
36	1250.5	76.1	387	2	AAR90920	Aar90920	IL4.Y124D
37	1249	76.0	252	6	ABJ38342	Abj38342	TALL-1 in
38	1249	76.0	528	4	AAE13061	Aae13061	ADAM-29di
39	1248.5	76.0	503	6	ABP72602	Abp72602	Human LP2
40	1248.5	76.0	535	2	AAy17414	Aay17414	SVPH1-26
41	1248.5	76.0	535	4	AAE13056	Aae13056	ADAM-20di
42	1248	76.0	287	4	AAB47590	Aab47590	Fusion pr
43	1248	76.0	358	6	ABP98040	Abp98040	Amino aci
44	1247	75.9	380	5	AAU97114	Aau97114	Human MK6
45	1246.5	75.9	717	6	ABP72600	Abp72600	Human LP2

ALIGNMENTS

RESULT 1

AAB60699

ID AAB60699 standard; protein; 302 AA.

XX

AC AAB60699;

XX

DT 11-SEP-2003 (revised)

DT 22-MAY-2001 (first entry)

XX

DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.

XX

KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

KW immune-related disorder; B-cell growth inhibitor;

KW B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

KW renal disorder; immunosuppressive disorder; HIV infection;

KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US022507.
 XX
 PR 17-AUG-1999; 99US-0149378P.
 PR 11-FEB-2000; 2000US-0181684P.
 PR 18-FEB-2000; 2000US-0183536P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTECH R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 PI Thompson J;
 XX
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF59999.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 XX
 PS Example 4; Fig 2; 59pp; English.
 XX
 CC The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human

CC BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 302 AA;

Query Match 100.0%; Score 1643; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 METDTLLLWVLLLWVPGSTGDVTMLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTC 60
      |||
Db      1 METDTLLLWVLLLWVPGSTGDVTMLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTC 60

Qy     61 QRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 120
      |||
Db     61 QRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 120

Qy    121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180
      |||
Db    121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180

Qy    181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240
      |||
Db    181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240

Qy    241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 300
      |||
Db    241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 300

Qy    301 GK 302
      ||
Db    301 GK 302
```

RESULT 2

AAE00507

ID AAE00507 standard; protein; 302 AA.

XX

AC AAE00507;

XX

DT 11-SEP-2003 (revised)

DT 31-JUL-2001 (first entry)

XX

DE Human BCMA-Immunoglobulin G Fc region fusion construct.

XX

KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
KW immunoglobulin G; IgG; Fc region.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX
 FH Key Location/Qualifiers
 FT Protein 1. .22
 FT /label= Signal_peptide
 FT /note= "Derived from murine Ig kappa sequence"
 FT Protein 23. .302
 FT /label= Mature_human_BCMA_IgG_Fc_fusion_protein
 FT Region 23. .75
 FT /note= "Derived from human BCMA protein"
 FT Domain 24. .302
 FT /label= Cysteine_rich_domain
 FT /note= "Derived from human BCMA"
 FT Region 76. .302
 FT /note= "Derived from human IgG Fc region"
 XX
 PN WO200124811-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027579.
 XX
 PR 06-OCT-1999; 99US-0157933P.
 PR 11-FEB-2000; 2000US-0181807P.
 PR 30-JUN-2000; 2000US-0215688P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTECH R & D SA.
 XX
 PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 XX
 DR WPI; 2001-266242/27.
 DR N-PSDB; AAD03847.
 XX
 PT Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 PT antagonist.
 XX
 PS Example 1; Fig 3B; 85pp; English.
 XX
 CC The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or carcinoma.
 CC The method involves administering a composition comprising A
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
 CC maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is a fusion construct containing human APRIL-R also referred as BCMA or

CC BCM protein, Fc region of human immunoglobulin G (IgG) and a signal
 CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 302 AA;

Query Match 100.0%; Score 1643; DB 4; Length 302;
 Best Local Similarity 100.0%; Pred. No. 1.4e-111;
 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	METD	11	WVLL	11	WVPG	11	STGD	11	VTML	11	QMA	11	GQCS	11	QNEY	11	FDSL	11	LHAC	11	IPCQ	11	LRCS	11	SNTP	11	PLTC	60
Db	1	METD	11	WVLL	11	WVPG	11	STGD	11	VTML	11	QMA	11	GQCS	11	QNEY	11	FDSL	11	LHAC	11	IPCQ	11	LRCS	11	SNTP	11	PLTC	60
Qy	61	QRYC	11	NASV	11	TNSV	11	KGVD	11	KTHC	11	PPCP	11	APEL	11	LLGG	11	PSVF	11	LFPP	11	PKPK	11	DTLM	11	ISRT	11	PEVT	120
Db	61	QRYC	11	NASV	11	TNSV	11	KGVD	11	KTHC	11	PPCP	11	APEL	11	LLGG	11	PSVF	11	LFPP	11	PKPK	11	DTLM	11	ISRT	11	PEVT	120
Qy	121	VSHD	11	PEVK	11	FNWY	11	VDG	11	VEVH	11	NAKT	11	KPRE	11	EQYN	11	STYR	11	VSVL	11	TVLH	11	QDWL	11	NGKE	11	YKCK	180
Db	121	VSHD	11	PEVK	11	FNWY	11	VDG	11	VEVH	11	NAKT	11	KPRE	11	EQYN	11	STYR	11	VSVL	11	TVLH	11	QDWL	11	NGKE	11	YKCK	180
Qy	181	KALP	11	APIE	11	KTIK	11	AKGQ	11	PREP	11	QVYT	11	LPSP	11	SRDE	11	LTKN	11	QVSL	11	TCLV	11	KGFY	11	PSDI	11	AVEW	240
Db	181	KALP	11	APIE	11	KTIK	11	AKGQ	11	PREP	11	QVYT	11	LPSP	11	SRDE	11	LTKN	11	QVSL	11	TCLV	11	KGFY	11	PSDI	11	AVEW	240
Qy	241	QPEN	11	NYKT	11	TPPV	11	LDSD	11	GSFF	11	LYSK	11	LTV	11	DKSR	11	WQQG	11	NVFS	11	CSVM	11	MHEA	11	LHNH	11	YTQK	300
Db	241	QPEN	11	NYKT	11	TPPV	11	LDSD	11	GSFF	11	LYSK	11	LTV	11	DKSR	11	WQQG	11	NVFS	11	CSVM	11	MHEA	11	LHNH	11	YTQK	300
Qy	301	GK	302																										
Db	301	GK	302																										

RESULT 3

AAE15488

ID AAE15488 standard; protein; 283 AA.

XX

AC AAE15488;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human BCMA-immunoglobulin Fc region fusion protein.

XX

KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.

XX

OS Homo sapiens.

XX

PN WO200187979-A2.

XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theill LE, Yu G;
XX
DR WPI; 2002-066686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
PS Disclosure; Fig 10B; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX
SQ Sequence 283 AA;

Query Match 90.6%; Score 1488.5; DB 5; Length 283;
Best Local Similarity 97.2%; Pred. No. 2.3e-100;
Matches 275; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 27 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
|||||
Db 1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAGGGGGGDKTH 60
QY 80 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139
|||||
Db 61 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 120
QY 140 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199

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      |||
Db      121 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 180
      |||
Qy      200 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
      |||
Db      181 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 240
      |||
Qy      260 FLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 302
      |||
Db      241 FLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 283

```

RESULT 4

AAE15489

ID AAE15489 standard; protein; 281 AA.

XX

AC AAE15489;

XX

DT 29-AUG-2003 (revised)

DT 12-MAR-2002 (first entry)

XX

DE Mouse BCMA-human immunoglobulin Fc region fusion protein.

XX

KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX

PN WO200187979-A2.

XX

PD 22-NOV-2001.

XX

PF 14-MAY-2001; 2001WO-US015567.

XX

PR 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX

PA (AMGE-) AMGEN INC.

XX

PI Theill LE, Yu G;

XX

DR WPI; 2002-066686/09.

XX

PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX

DT 02-MAY-2002 (first entry)
 XX
 DE Protein of hTACI (32-114)-IgG1 Fc.
 XX
 KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
 KW lung fibrosis; uterine; a proliferation inducing ligand; chimeric;
 KW hTACI(32-114)-IgG1 Fc.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .22
 FT /note= "Signal peptide from murine IgG-kappa"
 FT Domain 23. .105
 FT /label= Extracellular_domain
 FT /note= "Human TACI extracellular domain"
 FT Region 106. .334
 FT /note= "hIgG1 Fc sequence"
 XX
 PN WO200181417-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US040626.
 XX
 PR 27-APR-2000; 2000US-0199946P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Ambrose C, Thompson J, Schneider P, Rennert P;
 XX
 DR WPI; 2002-062027/08.
 DR N-PSDB; AAK98729.
 XX
 PT Treating mammal for condition associated with undesired cell
 PT proliferation e.g., solid tumor or reducing solid tumor size located in
 PT mammal comprises administering transmembrane activator CAML interactor
 PT protein reagent.
 XX
 PS Example; Fig 4; 42pp; English.
 XX
 CC This sequence represents the protein of a human TACI extracellular domain
 CC with a truncated stalk region initiating after the second methionine
 CC fused to human IgG Fc (hTACI(32-114)-IgG1 Fc). The signal sequence from
 CC murine IgG-kappa was fused in frame with the human TACI extracellular
 CC domain. The invention relates to treating a mammal for a condition
 CC associated with undesired cell proliferation (e.g. a solid tumour, or
 CC reducing the size of a solid tumour located on or in a mammal) comprising
 CC administering a transmembrane activator CAML interactor protein (TACI)

CC reagent. The TACI reagent has cytostatic and vulnerary activity. Treating
 CC a mammal (e.g. human, cow, horse, dog, mouse, rat or cat) for a condition
 CC associated with undesired cell proliferation (e.g. cancer such as renal
 CC cell cancer, Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma,
 CC rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer,
 CC mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous
 CC cell carcinoma, gastrointestinal cancer or stomach cancer). The method is
 CC also useful for treating cellular hyperproliferation (hyperplasia) such
 CC as scleroderma, pannus formation in rheumatoid arthritis, post-surgical
 CC scarring and lung, liver and uterine fibrosis. The TACI reagent of the
 CC invention can extend mean survival time of a mammal by 25% as compared to
 CC the mean survival time of a mammal in the absence of administering the
 CC TACI reagent. The TACI reagent also reduces the size of the tumour by 25%
 CC or more. (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 334 AA;

Query Match 83.9%; Score 1379; DB 5; Length 334;
 Best Local Similarity 77.1%; Pred. No. 2.7e-92;
 Matches 262; Conservative 10; Mismatches 24; Indels 44; Gaps 3;

Qy	1	METDTLLLLWVLLLWVPGSTGDTVMLQMAGQCSQNEYFDSLHACIPCQLRCSSNTP----	56
		: : : : :	
Db	1	METDTLLLLWVLLLWVPGSTGDVR-----SCPEEQYWDPLLGTCSCKTICNHQSQRTCA	54
Qy	57	-----PLTCQRYCNASVTNSVK-GVDKTHTCP	82
		: : :	
Db	55	AFCRSLSCRKEQGKFYDHLRLDCISCASICGQHPKQCAFCENKLRSFVNLFPVDKTHTCP	114
Qy	83	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	142
Db	115	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	174
Qy	143	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ	202
Db	175	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ	234
Qy	203	VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	262
Db	235	VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	294
Qy	263	SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	302
Db	295	SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	334

RESULT 6

AAO14132

ID AAO14132 standard; protein; 366 AA.

XX

AC AAO14132;

XX

DT 29-AUG-2003 (revised)

DT 02-MAY-2002 (first entry)

XX

DE Protein of hTACI (1-114)-IgG1.

XX

KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;
KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KW lung fibrosis; uterine; a proliferation inducing ligand; hIgG1 Fc; IgG1;
KW hTACI; chimeric.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Peptide 1. .23

FT /note= "Signal peptide from murine IgG-kappa"

FT Domain 24. .137

FT /label= Extracellular_domain

FT /note= "Human TACI extracellular domain"

FT Region 138. .366

FT /note= "hIgG1 Fc sequence"

XX

PN WO200181417-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US040626.

XX

PR 27-APR-2000; 2000US-0199946P.

XX

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTECH R & D SA.

XX

PI Ambrose C, Thompson J, Schneider P, Rennert P;

XX

DR WPI; 2002-062027/08.

DR N-PSDB; AAK98728.

XX

PT Treating mammal for condition associated with undesired cell

PT proliferation e.g., solid tumor or reducing solid tumor size located in

PT mammal comprises administering transmembrane activator CAML interactor

PT protein reagent.

XX

PS Disclosure; Fig 3; 42pp; English.

XX

CC This sequence represents the protein of a human TACI extracellular domain

CC with a truncated stalk region fused to human IgG Fc, called hTACI (1-114)

CC -IgG1. The signal sequence from murine IgG-kappa was fused in frame with

CC the human TACI extracellular domain. The invention relates to treating a

CC mammal for a condition associated with undesired cell proliferation (e.g.

CC a solid tumour, or reducing the size of a solid tumour located on or in a

CC mammal) comprising administering a transmembrane activator CAML

CC interactor protein (TACI) reagent. The TACI reagent has cytostatic and

CC vulnery activity. Treating a mammal (e.g. human, cow, horse, dog,

CC mouse, rat or cat) for a condition associated with undesired cell

CC proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma,

CC breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer,

CC melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary
 CC adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal
 CC cancer or stomach cancer). The method is also useful for treating
 CC cellular hyperproliferation (hyperplasia) such as scleroderma, pannus
 CC formation in rheumatoid arthritis, post-surgical scarring and lung, liver
 CC and uterine fibrosis. The TACI reagent of the invention can extend mean
 CC survival time of a mammal by 25% as compared to the mean survival time of
 CC a mammal in the absence of administering the TACI reagent. The TACI
 CC reagent also reduces the size of the tumour by 25% or more. (Updated on
 CC 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 366 AA;

Query Match 83.7%; Score 1376; DB 5; Length 366;
 Best Local Similarity 72.1%; Pred. No. 5e-92;
 Matches 264; Conservative 11; Mismatches 27; Indels 64; Gaps 3;

```

Qy      1 METDTLLLWVLLLWVPGSTGDVTMLQMA-----GQCSQN 34
      |||||
Db      1 METDTLLLWVLLLWVPGSTGDVTMSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEE 60

Qy     35 EYFDSLHACIPCQLRCSSNTP-----P 57
      :|:| || |: |: |: :
Db     61 QYWDPELLGTCMSCKTICNHQSQRTCAAFCSRSLSCRKEQGKFYDHLRDCISCASICGQHP 120

Qy     58 LTCQRYCNASVTNSVK-GVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 116
      | :| : : | |||||
Db    121 KQCAYFCENKLRSFVNLPVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 180

Qy    117 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 176
      |||||
Db    181 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 240

Qy    177 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 236
      |||||
Db    241 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 300

Qy    237 ESNQGPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 296
      |||||
Db    301 ESNQGPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 360

Qy    297 SLSPGK 302
      |||||
Db    361 SLSPGK 366
  
```

RESULT 7

AAE22245

ID AAE22245 standard; protein; 320 AA.

XX

AC AAE22245;

XX

DT 29-AUG-2003 (revised)

DT 25-JUL-2002 (first entry)

XX

DE Murine IgG-kappa signal sequence-human BAFF-R:Fc fusion protein.

XX

KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 KW murine; immunoglobulin G; IgG; fusion protein.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .21
 FT /label= Signal_peptide
 FT /note= "Murine IgG-kappa signal sequence"
 FT Protein 22. .320
 FT /note= "Mature human BAFF-R:Fc protein"
 FT Misc-difference 22
 FT /note= "Encoded by region introducing restriction site"
 FT Domain 23. .92
 FT /note= "Human BAFF-R extracellular domain"
 FT Misc-difference 93
 FT /note= "Encoded by region introducing restriction site"
 FT Region 94. .320
 FT /note= "Human IgG1 Fc region"
 XX
 PN WO200224909-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-US028006.
 XX
 PR 18-SEP-2000; 2000US-0233152P.
 PR 21-SEP-2000; 2000US-0234140P.
 PR 13-FEB-2001; 2001US-0268499P.
 PR 14-AUG-2001; 2001US-0312185P.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Ambrose CM, Thompson JS;
 XX
 DR WPI; 2002-362428/39.
 DR N-PSDB; AAD35412.
 XX
 PT New human BAFF receptor proteins and nucleic acids, useful for treating,
 PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
 PT genetic disorders involving B-cells, cardiovascular disorders, or renal
 PT disorders.
 XX
 PS Example 9; Fig 9; 164pp; English.
 XX
 CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are

useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopaenia purpura, Chagas' disease Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Waldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is a fusion protein containing murine IgG-kappa signal sequence linked to human BAFF-R and human immunoglobulin G (IgG) Fc region. (Updated on 29-AUG-2003 to standardise OS field)

Query Match 82.8%; Score 1361; DB 5; Length 320;
Best Local Similarity 82.2%; Pred. No. 5.2e-91;
Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

RESULT 8
ABR55865
ID ABR55865 standard; protein; 320 AA.
XX

AC ABR55865;
 XX
 DT 02-SEP-2003 (first entry)
 XX
 DE Human immunoglobulin G (IgG) Fc portion.
 XX
 KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
 KW immunoglobulin G; IgG; Fc; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003031464-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 09-OCT-2002; 2002WO-US032263.
 XX
 PR 10-OCT-2001; 2001US-0328523P.
 PR 19-OCT-2001; 2001US-0344692P.
 PR 28-NOV-2001; 2001US-0334233P.
 PR 28-NOV-2001; 2001US-0334301P.
 PR 07-JUN-2002; 2002US-0387292P.
 PR 25-JUN-2002; 2002US-0391777P.
 PR 17-JUL-2002; 2002US-0396594P.
 PR 16-AUG-2002; 2002US-0404249P.
 PR 28-AUG-2002; 2002US-0407527P.
 XX
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 XX
 PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
 XX
 DR WPI; 2003-449162/42.
 DR N-PSDB; ACC78891.
 XX
 PT Remodeling a peptide, by removing a saccharyl subunit from the peptide to
 PT form truncated glycan, and adding or deleting glycosyl groups to a
 PT peptide and/or adding modifying group of a peptide to remodel the
 PT peptide.
 XX
 PS Example; Fig 75B; 900pp; English.
 XX
 CC The invention relates to a cell-free, in vitro method of remodeling a
 CC peptide. The method involves removing a saccharyl subunit from the
 CC peptide, thus forming a truncated glycan, and contacting the truncated
 CC glycan with at least one glycosyltransferase and at least one glycosyl
 CC donor under conditions suitable to transfer at least one glycosyl donor
 CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
 CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
 CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
 CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
 CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
 CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
 CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
 CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
 CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
 CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2
 CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-

CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
 CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
 CC hormone (HGH) peptide, and a modifying group, where the modifying group
 CC is covalently attached to the peptide through an intact glycosyl linking
 CC group. The method is useful for a cell-free, in vitro method of
 CC remodeling the above mentioned peptides. The present sequence represents
 CC a human immunoglobulin G (IgG) Fc portion
 XX
 SQ Sequence 320 AA;

Query Match 82.8%; Score 1361; DB 6; Length 320;
 Best Local Similarity 82.2%; Pred. No. 5.2e-91;
 Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

Qy	1	METDTLLLWVLLLVPGSTGDVTM--LQMAQQ-----CSQNEYFDSLHACIPCQL--	49
		: : : :	
Db	1	METDTLLLWVLLLVPGSTGDVRRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLR	60
Qy	50	-----RCSSNTPPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPPELLGGPSVFLFPPKP	102
		:	
Db	61	TPRPKPAGASSPAPRTALQPQESVGAGAGEAAVDKTHTCPPCPAPPELLGGPSVFLFPPKP	120
Qy	103	KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT	162
Db	121	KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT	180
Qy	163	VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT	222
Db	181	VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT	240
Qy	223	LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC	282
Db	241	LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC	300
Qy	283	MHEALHNHYTQKSLSLSPGK	302
Db	301	MHEALHNHYTQKSLSLSPGK	320

RESULT 9

AAE35228

ID AAE35228 standard; protein; 332 AA.

XX

AC AAE35228;

XX

DT 23-OCT-2003 (revised)

DT 28-MAY-2003 (first entry)

XX

DE Human TACI-Fc5 fusion protein comprising murine 26-10 VH signal peptide.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;

Db 122 APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 181
 Qy 152 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 211
 |||||||||||||||||||||||||||||||||||: ||||||||||||||||||||||||
 Db 182 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSRD 241
 Qy 212 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 271
 |||||||||||||||||||||||||||||||||||
 Db 242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 301
 Qy 272 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
 ||||||||||||||||||||||||||||||||
 Db 302 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332

RESULT 10

AAE13055

ID AAE13055 standard; protein; 446 AA.

XX

AC AAE13055;

XX

DT 28-JAN-2002 (first entry)

XX

DE ADAM-17dis-Fc fusion construct.

XX

KW Human; ADAM disintegrin domain; integrin; endothelial cell migration;
 KW angiogenesis; ocular disorder; inflammatory disease; bone resorption;
 KW osteoporosis; restenosis; thrombosis; tissue repair; wound healing;
 KW retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
 KW retrolental fibroplasia; inflammatory bowel disease; rubeosis; uveitis;
 KW arthritis; rheumatism; myocardial infarction; coronary artery disease;
 KW tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;
 KW preeclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;
 KW IgK; Fc region; antiinflammatory; osteopathic; vasotropic; thrombolytic.

XX

OS Homo sapiens.

OS Unidentified.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Peptide 1. .20

FT /label= IgK_leader_sequence

FT Protein 21. .446

FT /note= "Mature ADAM-17dis-Fc fusion construct"

FT Region 23. .216

FT /note= "Human ADAM disintegrin"

FT Domain 34. .93

FT /label= Human_ADAM_disintegrin_domain

FT Region 219. .446

FT /note= "Fc region"

XX

PN WO200162905-A2.

XX

PD 30-AUG-2001.

XX

PF 23-FEB-2001; 2001WO-US005701.

XX

PR 25-FEB-2000; 2000US-0184865P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Fanslow WC, Cerretti DP, Poindexter KM, Black RA;

XX

DR WPI; 2001-625725/72.

DR N-PSDB; AAD21435.

XX

PT Antagonizing the binding of an integrin to its ligand useful for the
PT treatment of angiogenesis comprises administration of an ADAM-disintegrin
PT domain polypeptide.

XX

PS Claim 11; Page 46-47; 66pp; English.

XX

CC The invention relates to the method and use of ADAM disintegrin domain
CC polypeptides for inhibiting the biological activity of integrins,
CC endothelial cell migration and angiogenesis. ADAM disintegrin domain
CC polypeptides are used for treatment of ocular disorders, malignant and
CC metastatic conditions, inflammatory diseases, osteoporosis and other
CC conditions mediated by accelerated bone resorption, restenosis,
CC inappropriate platelet activation, recruitment or aggregation, thrombosis
CC or a condition requiring aggregation, thrombosis or a condition requiring
CC tissue repair or wound healing, angiogenesis, ocular neovascularisation
CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,
CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubeosis,
CC uveitis, macular degeneration and corneal graft neovascularisation,
CC inflammatory diseases, ocular tumours, diseases associated with choroidal
CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel
CC disease, psoriasis, coronary artery disease or injury, myocardial
CC infarction or injury following myocardial infarction, stroke, unstable
CC angina, atherosclerosis, arteriosclerosis, preeclampsia, embolism,
CC platelet-associated ischaemic disorders including lung ischaemia,
CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
CC coronary intervention including angioplasty, atherectomy, stent placement
CC and bypass surgery, thrombotic disorders including coronary artery
CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis and
CC coagulopathies associated with exposure to a foreign or injured tissue
CC surface and reocclusion following thrombosis, deep venous thrombosis,
CC pulmonary embolism, transient ischaemic attacks and another conditions
CC where vascular occlusion is a common underlying feature, in individuals
CC at high risk for thrombus formation of reformation, advanced coronary
CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis
CC of blood vessels or stroke benign tumours and preneoplastic conditions,
CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular
CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host
CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and
CC wound granulation. The method are used in combination with angioplasty
CC procedures, such as balloon angioplasty, laser angioplasty, coronary
CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of
CC vascular grafts, surgery having a high risk of thrombus formation (i.e.
CC coronary bypass surgery, insertion of a prosthetic valve or vessel and
CC the like), atherectomy, stent placement, placement of a chronic
CC cardiovascular device such as an in-dwelling catheter or prosthetic valve
CC or vessel, organ transplantation or bypass surgery. The present sequence
CC is ADAM disintegrin domain polypeptide fusion construct. The fusion

CC construct comprises of immunoglobulin K (IgK) leader, human ADAM
CC disintegrin and Fc region
XX
SQ Sequence 446 AA;

Query Match 77.2%; Score 1269; DB 4; Length 446;
Best Local Similarity 57.2%; Pred. No. 3.9e-84;
Matches 261; Conservative 2; Mismatches 29; Indels 164; Gaps 5;

```
Qy      1 METDTLLLWVLLLWVPGSTG-----DVTMLQMAQC 31
      |||
Db      1 METDTLLLWVLLLWVPGSTGTSCGNSRVDEGEEDPGIMYLNNDTCCNSDCT-LKEGVQC 59

Qy     32 SQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNAS----- 67
      |
Db     60 SDRN-----SPCKKNCQFETAQKKCQEAINATCKGVSCTGNSSECPPPGNAEDDT 110

Qy     68 -----VTNSVK----- 73
      ||
Db    111 VCLDLGKCKDGKCI PFCEREQQLESCACNETDNSCKVCCRDLSGRCPYVDAEQKNLFLR 170

Qy     74 -----GVDKTHTCPPCPA 86
      |||
Db    171 KGKPCTVGFCDMNGKCEKRVQDVIERFWDFIDQLSINTFGKFLADNRSCDKTHTCPPCPA 230

Qy     87 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 146
      ||
Db    231 PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 290

Qy    147 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 206
      |||
Db    291 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 350

Qy    207 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 266
      |||
Db    351 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 410

Qy    267 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
      |||
Db    411 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 446
```

RESULT 11

AA Y84965

ID AAY84965 standard; protein; 633 AA.

XX

AC AAY84965;

XX

DT 21-AUG-2000 (first entry)

XX

DE Amino acid sequence of a CD-20 specific chimeric receptor.

XX

KW CD20-specific receptor; CD-20 specific redirected T cell; leukemia;

KW CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;

KW stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis.

XX

OS Synthetic.

OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 21. .126
 FT /note= "anti-CD20 variable regions"
 FT Peptide 27. .86
 FT /note= "signal peptide from murine T86.66 antibody kappa
 FT light chain"
 FT Peptide 145. .266
 FT /note= "GS18 linker"
 FT Region 283. .392
 FT /note= "hinge region"
 FT Region 393. .499
 FT /note= "CH3 region"
 FT Region 500. .521
 FT /note= "CD4 transmembrane region"
 FT Region 522. .633
 FT /note= "zeta chain"
 XX
 PN WO200023573-A2.
 XX
 PD 27-APR-2000.
 XX
 PF 20-OCT-1999; 99WO-US024484.
 XX
 PR 20-OCT-1998; 98US-0105014P.
 XX
 PA (CITY) CITY OF HOPE.
 XX
 PI Raubitschek A, Jensen MC, Wu AM;
 XX
 DR WPI; 2000-339676/29.
 DR N-PSDB; AAA15019.
 XX
 PT Genetically engineered CD20-specific redirected T cells useful for
 PT treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+
 PT acute or chronic leukemia, and autoimmune disease.
 XX
 PS Claim 10; Page 53-55; 58pp; English.
 XX
 CC The present sequence represents a synthetic CD20-specific chimeric
 CC receptor. The specification describes CD-20 specific redirected T cells
 CC which express and bear on the cell surface membrane a CD20-chimeric
 CC receptor comprising an intracellular signalling domain, a transmembrane
 CC domain and an extracellular domain, the extracellular domain comprising a
 CC CD20-specific receptor. The genetically engineered CD20-specific
 CC redirected T cells are useful for treating a CD20+ malignancy, such as
 CC non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a human
 CC patient having previously undergone myeloablative chemotherapy and stem
 CC cell rescue. The genetically engineered CD20-specific redirected T cells
 CC are also useful for abrogating an untoward B cell function, such as
 CC autoimmune disease (lupus or rheumatoid arthritis) in a patient
 XX
 SQ Sequence 633 AA;

Query Match 77.2%; Score 1268.5; DB 3; Length 633;
 Best Local Similarity 53.1%; Pred. No. 6.4e-84;

```

Matches 265; Conservative 9; Mismatches 28; Indels 197; Gaps 5;

Qy      1 METDTLLLWVLLLWVPGSTGDVTMLQ MAGQCSQNE----- 35
      |||||:|:|
Db      1 METDTLLLWVLLLWVPGSTGDIVLTQSPAILSASPGEKVTMTCRASSSVNYMDWYQKKPG 60

Qy      36 -----YFDSLHACIP-----CQ----- 48
      | | | : : |
Db      61 SSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPPTFGGG 120

Qy      49 ----- 48

Db      121 TKLEIKGSTSGGGSGGGSGGGSSSEVQLQQSGAELVKPGASVKMSCKASGYTFTSYNMHW 180

Qy      49 -----LRCSSNTPPLTCQRYC 64
      :: || | : ||
Db      181 VKQTPGQGLEWIGAIYPNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSADYYC 240

Qy      65 -----NASVTNSV-----KGVDKTHTCPPCPAPELLGGPSVFLFPPKPK 103
      | | : | | |||||
Db      241 ARSNYYGSSYWFFDVWGAGTTVTVSSSLDPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPK 300

Qy      104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
      |||||
Db      301 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 360

Qy      164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
      |||||
Db      361 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 420

Qy      224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 283
      |||||
Db      421 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 480

Qy      284 HEALHNHYTQKSLSLSPGK 302
      |||||
Db      481 HEALHNHYTQKSLSLSPGK 499

```

RESULT 12

AAE13053

ID AAE13053 standard; protein; 465 AA.

XX

AC AAE13053;

XX

DT 28-JAN-2002 (first entry)

XX

DE ADAM-10dis-Fc fusion construct.

XX

KW Human; ADAM disintegrin domain; integrin; endothelial cell migration;
 KW angiogenesis; ocular disorder; inflammatory disease; bone resorption;
 KW osteoporosis; restenosis; thrombosis; tissue repair; wound healing;
 KW retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
 KW retrolental fibroplasia; inflammatory bowel disease; rubeosis; uveitis;
 KW arthritis; rheumatism; myocardial infarction; coronary artery disease;
 KW tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;
 KW preeclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;

KW IgK; Fc region; antiinflammatory; osteopathic; vasotropic; thrombolytic.
 XX
 OS Homo sapiens.
 OS Unidentified.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .20
 FT /label= IgK_leader_sequence
 FT Protein 21. .465
 FT /note= "Mature ADAM-10dis-Fc fusion construct"
 FT Region 23. .235
 FT /note= "Human ADAM disintegrin"
 FT Domain 34. .99
 FT /label= Human_ADAM_disintegrin_domain
 FT Region 238. .465
 FT /note= "Fc region"
 XX
 PN WO200162905-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005701.
 XX
 PR 25-FEB-2000; 2000US-0184865P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Fanslow WC, Cerretti DP, Poindexter KM, Black RA;
 XX
 DR WPI; 2001-625725/72.
 DR N-PSDB; AAD21433.
 XX
 PT Antagonizing the binding of an integrin to its ligand useful for the
 PT treatment of angiogenesis comprises administration of an ADAM-disintegrin
 PT domain polypeptide.
 XX
 PS Claim 11; Page 40-41; 66pp; English.
 XX
 CC The invention relates to the method and use of ADAM disintegrin domain
 CC polypeptides for inhibiting the biological activity of integrins,
 CC endothelial cell migration and angiogenesis. ADAM disintegrin domain
 CC polypeptides are used for treatment of ocular disorders, malignant and
 CC metastatic conditions, inflammatory diseases, osteoporosis and other
 CC conditions mediated by accelerated bone resorption, restenosis,
 CC inappropriate platelet activation, recruitment or aggregation, thrombosis
 CC or a condition requiring aggregation, thrombosis or a condition requiring
 CC tissue repair or wound healing, angiogenesis, ocular neovascularisation
 CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,
 CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubeosis,
 CC uveitis, macular degeneration and corneal graft neovascularisation,
 CC inflammatory diseases, ocular tumours, diseases associated with choroidal
 CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel
 CC disease, psoriasis, coronary artery disease or injury, myocardial
 CC infarction or injury following myocardial infarction, stroke, unstable
 CC angina, atherosclerosis, arteriosclerosis, preeclampsia, embolism,
 CC platelet-associated ischaemic disorders including lung ischaemia,

CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
 CC coronary intervention including angioplasty, atherectomy, stent placement
 CC and bypass surgery, thrombotic disorders including coronary artery
 CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis and
 CC coagulopathies associated with exposure to a foreign or injured tissue
 CC surface and reocclusion following thrombosis, deep venous thrombosis,
 CC pulmonary embolism, transient ischaemic attacks and another conditions
 CC where vascular occlusion is a common underlying feature, in individuals
 CC at high risk for thrombus formation of reformation, advanced coronary
 CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis
 CC of blood vessels or stroke benign tumours and preneoplastic conditions,
 CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular
 CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host
 CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and
 CC wound granulation. The method are used in combination with angioplasty
 CC procedures, such as balloon angioplasty, laser angioplasty, coronary
 CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of
 CC vascular grafts, surgery having a high risk of thrombus formation (i.e.
 CC coronary bypass surgery, insertion of a prosthetic valve or vessel and
 CC the like), atherectomy, stent placement, placement of a chronic
 CC cardiovascular device such as an in-dwelling catheter or prosthetic valve
 CC or vessel, organ transplantation or bypass surgery. The present sequence
 CC is ADAM disintegrin domain polypeptide fusion construct. The fusion
 CC construct comprises of immunoglobulin K (IgK) leader, human ADAM
 CC disintegrin and Fc region
 XX
 SQ Sequence 465 AA;

Query Match 77.0%; Score 1265.5; DB 4; Length 465;
 Best Local Similarity 56.1%; Pred. No. 7.3e-84;
 Matches 261; Conservative 11; Mismatches 30; Indels 163; Gaps 7;

Qy	1	METDTLLLWVLLLVPGSTG-----DVTM-----L	25
Db	1	METDTLLLWVLLLVPGSTGTSCNGMVEQGEEDCGYSDQCKDECCFDANQPEGRKCKL	60
Qy	26	QMAGQCSQNE-----YFDSLHACIP-----	46
		: :: :	
Db	61	KPGKQCSQSPQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALCPASDEKPNFTDCNR	120
Qy	47	-----CQLRCSSNTPPLTC-----	60
		:	
Db	121	HTQVCINGQCAGSICEKYGLEECTCASSDGKDDKELCHVCCMKMDPSTCASTGSVQWSR	180
Qy	61	-----QRYCN-----ASVTNSV-----KGVDK	77
		: : : :: :	
Db	181	HFSGRITITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAI FSPELYENIAERSCDK	240
Qy	78	THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV	137
Db	241	THTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV	300
Qy	138	EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ	197
Db	301	EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ	360

Qy 198 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 257
 |||
 Db 361 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 420
 Qy 258 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
 |||
 Db 421 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465

RESULT 13

AAO14136

ID AAO14136 standard; protein; 404 AA.

XX

AC AAO14136;

XX

DT 29-AUG-2003 (revised)

DT 02-MAY-2002 (first entry)

XX

DE Protein of a complete TACI extracellular domain fused to a human IgG-Fc.

XX

KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 KW cell proliferation; tumour; vulnerary; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
 KW lung fibrosis; uterine; IgG-Fc; chimeric.

XX

OS Homo sapiens.

OS Chimeric.

XX

PN WO200181417-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US040626.

XX

PR 27-APR-2000; 2000US-0199946P.

XX

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTECH R & D SA.

XX

PI Ambrose C, Thompson J, Schneider P, Rennert P;

XX

DR WPI; 2002-062027/08.

DR N-PSDB; AAK98732.

XX

PT Treating mammal for condition associated with undesired cell
 PT proliferation e.g., solid tumor or reducing solid tumor size located in
 PT mammal comprises administering transmembrane activator CAML interactor
 PT protein reagent.

XX

PS Example; Fig 5; 42pp; English.

XX

CC This sequence represents the protein of a complete extracellular domain
 CC of TACI fused to a human IgG-Fc. The invention relates to treating a
 CC mammal for a condition associated with undesired cell proliferation (e.g.

CC a solid tumour, or reducing the size of a solid tumour located on or in a
 CC mammal) comprising administering a transmembrane activator CAML
 CC interactor protein (TACI) reagent. The TACI reagent has cytostatic and
 CC vulnerary activity. Treating a mammal (e.g. human, cow, horse, dog,
 CC mouse, rat or cat) for a condition associated with undesired cell
 CC proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma,
 CC breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer,
 CC melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary
 CC adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal
 CC cancer or stomach cancer). The method is also useful for treating
 CC cellular hyperproliferation (hyperplasia) such as scleroderma, pannus
 CC formation in rheumatoid arthritis, post-surgical scarring and lung, liver
 CC and uterine fibrosis. The TACI reagent of the invention can extend mean
 CC survival time of a mammal by 25% as compared to the mean survival time of
 CC a mammal in the absence of administering the TACI reagent. The TACI
 CC reagent also reduces the size of the tumour by 25% or more. (Updated on
 CC 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 404 AA;

Query Match 77.0%; Score 1264.5; DB 5; Length 404;
 Best Local Similarity 77.7%; Pred. No. 7.3e-84;
 Matches 244; Conservative 6; Mismatches 19; Indels 45; Gaps 3;

Qy	33	QNEYFDSLLHACIPC-----QLRCSSNTPPLTCQRYCNASVTN-----	70
		::: : : :	
Db	92	QGKFYDHLRLDCISCASICGQHPKQCAVFCENKLRSPVNLPP-ELRRQRSGEVENNSDNS	150
Qy	71	-----SVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI	108
Db	151	GRYQGLEHRGSEASPALPGLKLSADQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI	210
Qy	109	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW	168
Db	211	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW	270
Qy	169	LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY	228
Db	271	LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY	330
Qy	229	PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALH	288
Db	331	PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALH	390
Qy	289	NHYTQKSLSLSPGK	302
Db	391	NHYTQKSLSLSPGK	404

RESULT 14
 AAE35225
 ID AAE35225 standard; protein; 348 AA.
 XX
 AC AAE35225;
 XX
 DT 28-MAY-2003 (first entry)
 XX

DE Human TACI(dl-29, dl111-154)-Fc5 variant construct protein.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW chimeric.

XX

OS Homo sapiens.

XX

PN WO200294852-A2.

XX

PD 28-NOV-2002.

XX

PF 20-MAY-2002; 2002WO-US015910.

XX

PR 24-MAY-2001; 2001US-0293343P.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Rixon MW, Gross JA;

XX

DR WPI; 2003-148455/14.

DR

XX

PT Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

XX

PS Claim 26; Col 129-130; 71pp; English.

XX

CC The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human TACI-Fc5 variant construct
CC protein

XX

SQ Sequence 348 AA;

Query Match 76.9%; Score 1263; DB 6; Length 348;

Best Local Similarity 86.7%; Pred. No. 7.9e-84;

Matches 234; Conservative 8; Mismatches 26; Indels 2; Gaps 1;

QY 33 QNEYFDSLHLHACIPCLRCSSNTPPLTLCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGG 92

|::| || || | : | : | : | |||||

Db 81 QGKFYDHLRLDCISCASICGQH--PKQCA YFCENKLRSEPKSSDKTHTCPPCPAPEAEGA 138

Qy	93	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	152
Db	139	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	198
Qy	153	STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	212
		:	
Db	199	STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSRDE	258
Qy	213	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	272
Db	259	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	318
Qy	273	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	302
Db	319	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	348

RESULT 15

ABJ37102

ID ABJ37102 standard; protein; 608 AA.

XX

AC ABJ37102;

XX

DT 08-MAY-2003 (first entry)

XX

DE Concatameric immunoadhesion human protein sequence SEQ ID No 10.

XX

KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
 KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
 KW dimeric protein; inflammation; septicemia; cytotoxicity;
 KW rheumatoid arthritis; cachexia; inflammation; human.

XX

OS Homo sapiens.

XX

PN WO2003010202-A1.

XX

PD 06-FEB-2003.

XX

PF 26-JUL-2002; 2002WO-KR001427.

XX

PR 26-JUL-2001; 2001KR-00045028.

XX

PA (MEDE-) MEDEXGEN CO LTD.

XX

PI Chung Y, Han J, Lee H, Choi E, Kim J;

XX

DR WPI; 2003-229639/22.

DR

N-PSDB; ABT32045.

XX

PT New concatameric protein having two soluble domains, useful for
 PT diagnosing and treating disorders associated with the dimeric protein or
 PT its glycosylated form, such as inflammation, septicemia, rheumatoid
 PT arthritis and cachexia.

XX

PS Claim 27; Page 139-142; 211pp; English.

XX

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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:19:08 ; Search time 20.5062 Seconds
(without alignments)
760.310 Million cell updates/sec

Title: PCT-US03-05147-3
Perfect score: 1643
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1264.5	77.0	398	4	US-09-612-033B-14	Sequence 14, Appl
2	1257.5	76.5	360	4	US-09-180-100-11	Sequence 11, Appl
3	1257.5	76.5	376	4	US-09-180-100-22	Sequence 22, Appl
4	1250.5	76.1	387	1	US-08-470-299-4	Sequence 4, Appli
5	1243	75.7	371	1	US-08-236-311-7	Sequence 7, Appli
6	1243	75.7	371	3	US-08-457-918-7	Sequence 7, Appli
7	1243	75.7	446	3	US-08-397-411-7	Sequence 7, Appli
8	1243	75.7	449	1	US-08-458-516-13	Sequence 13, Appli
9	1243	75.7	459	1	US-08-157-101A-7	Sequence 7, Appli
10	1243	75.7	476	2	US-08-378-939-10	Sequence 10, Appl
11	1243	75.7	547	4	US-09-746-359A-54	Sequence 54, Appl

12	1243	75.7	571	4	US-09-746-359A-53	Sequence 53, Appl
13	1243	75.7	951	4	US-09-313-942-9	Sequence 9, Appli
14	1241	75.5	331	3	US-09-178-869-2	Sequence 2, Appli
15	1241	75.5	331	4	US-09-761-413-2	Sequence 2, Appli
16	1240	75.5	482	4	US-09-189-129-2	Sequence 2, Appli
17	1239.5	75.4	347	1	US-07-940-861-43	Sequence 43, Appl
18	1239.5	75.4	347	1	US-08-459-512-43	Sequence 43, Appl
19	1239.5	75.4	347	2	US-08-459-657-43	Sequence 43, Appl
20	1239.5	75.4	347	2	US-08-460-132-43	Sequence 43, Appl
21	1239.5	75.4	347	3	US-08-466-465-8	Sequence 8, Appli
22	1239.5	75.4	347	5	PCT-US92-02050-43	Sequence 43, Appl
23	1239	75.4	462	4	US-09-289-942A-7	Sequence 7, Appli
24	1239	75.4	475	4	US-09-740-002-27	Sequence 27, Appl
25	1239	75.4	476	3	US-08-487-550-4	Sequence 4, Appli
26	1239	75.4	476	3	US-08-487-550-12	Sequence 12, Appl
27	1239	75.4	476	4	US-09-526-098-4	Sequence 4, Appli
28	1239	75.4	476	4	US-09-526-098-12	Sequence 12, Appl
29	1239	75.4	478	3	US-08-487-550-8	Sequence 8, Appli
30	1239	75.4	478	4	US-09-526-098-8	Sequence 8, Appli
31	1238.5	75.4	592	4	US-09-313-942-8	Sequence 8, Appli
32	1238	75.3	424	4	US-09-333-593A-8	Sequence 8, Appli
33	1238	75.3	446	4	US-09-157-452B-12	Sequence 12, Appl
34	1238	75.3	488	3	US-08-776-511-2	Sequence 2, Appli
35	1237	75.3	229	4	US-09-122-144-2	Sequence 2, Appli
36	1237	75.3	232	2	US-08-595-043A-50	Sequence 50, Appl
37	1237	75.3	330	4	US-09-301-593-22	Sequence 22, Appl
38	1237	75.3	396	2	US-08-784-512-3	Sequence 3, Appli
39	1237	75.3	396	3	US-09-176-228-3	Sequence 3, Appli
40	1237	75.3	424	5	PCT-US95-03866-12	Sequence 12, Appl
41	1237	75.3	424	5	PCT-US95-03866-14	Sequence 14, Appl
42	1237	75.3	437	5	PCT-US96-10043-11	Sequence 11, Appl
43	1237	75.3	442	4	US-08-472-888A-7	Sequence 7, Appli
44	1237	75.3	442	5	PCT-US96-10043-9	Sequence 9, Appli
45	1237	75.3	451	2	US-08-887-352B-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-612-033B-14

; Sequence 14, Application US/09612033B

; Patent No. 6627199

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: Isolation, Identification, and Characterization of

; TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily

; TITLE OF INVENTION: of Genes

; FILE REFERENCE: 01017/35434A

; CURRENT APPLICATION NUMBER: US/09/612,033B

; CURRENT FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14


```

;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
;   OTHER INFORMATION: consisting of Mus musculus sequences and
;   OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

```

RESULT 2

```

US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11

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Query Match 76.5%; Score 1257.5; DB 4; Length 360;
Best Local Similarity 84.8%; Pred. No. 6e-112;

	Matches	240;	Conservative	8;	Mismatches	20;	Indels	15;	Gaps	4;
Qy	30	QCSQNEYFDS-LLHACIPC-----QLRCSSTNPPLTCQRYCNASVTNSVKGV	DKTH	79						
Db	83	RCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSNT---KCKE--EGSRSNEPKSCDKTH	137							
Qy	80	TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	139							
Db	138	TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	197							
Qy	140	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	199							
Db	198	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	257							
Qy	200	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF	259							
Db	258	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF	317							
Qy	260	FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	302							
Db	318	FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	360							

Query Match 76.5%; Score 1257.5; DB 4; Length 376;
Best Local Similarity 84.8%; Pred. No. 6.3e-112;
Matches 240; Conservative 8; Mismatches 20; Indels 15; Gaps 4;

Db	214	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	273
Qy	200	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF	259
Db	274	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF	333
Qy	260	FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	302
Db	334	FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	376

RESULT 4

US-08-470-299-4

; Sequence 4, Application US/08470299

; Patent No. 5783181

; GENERAL INFORMATION:

; APPLICANT: Browne, Michael J.

; APPLICANT: Murphy, Kay E.

; APPLICANT: Chapman, Conrad G.

; APPLICANT: Clinkenbeard, Helen E.

; APPLICANT: Young, Peter R.

; APPLICANT: Shatzman, Allan R.

; TITLE OF INVENTION: No. 5783181el Compounds

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road, P.O. Box 1539

; CITY: King of Prussia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,299

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P31005C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5024

; TELEFAX: 610-270-5090

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-470-299-4

Query Match

76.1%; Score 1250.5; DB 1; Length 387;

QY 229 PSDIAVEWESNGQPENNYKTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 288
 |||||
 Db 298 PSDIAVEWESNGQPENNYKTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 357
 QY 289 NHYTQKSLSLSPGK 302
 |||||
 Db 358 NHYTQKSLSLSPGK 371

RESULT 7

US-08-397-411-7

; Sequence 7, Application US/08397411

; Patent No. 6129914

; GENERAL INFORMATION:

; APPLICANT: Weiner, George

; APPLICANT: Gingrich, Roger

; APPLICANT: Link, Brian

; APPLICANT: Tso, J. Yun

; TITLE OF INVENTION: Bispecific Antibody Effective to Treat

; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/397,411

; FILING DATE: 01-MAR-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/859,583

; FILING DATE: 27-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 011823-004901

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 446 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-397-411-7


```

Qy      289 NHYTQKSLSLSPGK 302
          |||||
Db      463 NHYTQKSLSLSPGK 476

```

```

RESULT 11
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

```

Query Match 75.7%; Score 1243; DB 4; Length 547;
Best Local Similarity 92.1%; Pred. No. 2.7e-110;
Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

[illegible]

Qy 289 NHYTQKSLSLSPGK 302
 |||||
 Db 534 NHYTQKSLSLSPGK 547

```

RESULT 12
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-53

```

Query Match 75.7%; Score 1243; DB 4; Length 571;
Best Local Similarity 92.1%; Pred. No. 2.8e-110;
Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

[illegible]

Qy 289 NHYTQKSLSLSPGK 302
| | | | | | | | | | | | | |
Db 558 NHYTQKSLSLSPGK 571

RESULT 13

US-09-313-942-9

; Sequence 9, Application US/09313942

; Patent No. 6472179

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

; CURRENT APPLICATION NUMBER: US/09/313,942

; CURRENT FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 09/313,942

; PRIOR FILING DATE: 1999-05-19

: PRIOR APPLICATION NUMBER: 60/101,858

; PRIOR FILING DATE: 1998-09-25

; NUMBER OF SEO ID NOS: 32

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; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEO ID NO 9

; LENGTH: 951

; TYPE: PRT

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; ORGANISM: Homo sapiens
```

US-09-313-942-9

Query Match 75.7%; Score 1243; DB 4; Length 951;

Best Local Similarity 92.1%; Pred. No. 6e-110;

Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

Qy 51 CSSNTPPLTCQRYCNASVTNSV--KGVDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 108
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 704 CNVNHKP-----SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 757

QY 109 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 168

Db 758 SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEOYNSTYRVVSVLTVLHQDW 817

QY 169 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 228

Db 818 LNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFY 877

QY 229 PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALH 288

Db 878 PS DIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWOOGNVFSCSVMHEALH 937

QY 289 NHYTQKSLSLSPGK 302
 |||||

Db 938 NHYTOKSLSLSPGK 951

RESULT 14

US-09-178-869-2

; Sequence 2, Application US/09178869B

```
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2
```

```
Query Match          75.5%; Score 1241; DB 3; Length 331;
Best Local Similarity 78.7%; Pred. No. 2e-110;
Matches 240; Conservative 9; Mismatches 30; Indels 26; Gaps 3;
```

```
Qy      20 GDVTMLQ MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQ----- 61
      || : ::| : | |: | : || : |
Db      31 GDNSHVEMKLAVDEEENADNNTKANVTKPKRCSGS----ICYGTVIAVIVFFLIGFMIGYL 86

Qy      62 RYCNA----SVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 117
      || : : | | |||||
Db      87 GYCKGVEPKTEGSEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 146

Qy     118 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 177
      |||||
Db     147 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 206

Qy     178 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 237
      |||||
Db     207 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 266

Qy     238 SNGQPENNYKTTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSVMSHEALHNHYTQKSLS 297
      |||||
Db     267 SNGQPENNYKTTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSVMSHEALHNHYTQKSLS 326

Qy     298 LSPGK 302
      |||||
Db     327 LSPGK 331
```

RESULT 15

US-09-761-413-2

```
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hammang, Joseph P.
```

```
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-413-2
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```
Query Match          75.5%; Score 1241; DB 4; Length 331;
Best Local Similarity 78.7%; Pred. No. 2e-110;
Matches 240; Conservative 9; Mismatches 30; Indels 26; Gaps 3;
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Qy      20 GDVTMLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ----- 61
      || : ::| : | | : | | : || : |
Db      31 GDNSHVEMKLAVDEEENADNNTKANVTKPKRCSGS----ICYGTVIAVIVFFLIGFMIGYL 86

Qy      62 RYCNA----SVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 117
      || : : | | |||||
Db      87 GYCKGVEPKTEGSEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 146

Qy     118 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 177
      |||||
Db     147 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 206

Qy     178 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 237
      |||||
Db     207 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 266

Qy     238 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 297
      |||||
Db     267 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 326

Qy     298 LSPGK 302
      ||||
Db     327 LSPGK 331
```

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Search completed: April 19, 2004, 13:24:21
Job time : 21.5062 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:18:32 ; Search time 16.7778 Seconds
(without alignments)
1731.447 Million cell updates/sec

Title: PCT-US03-05147-3
Perfect score: 1643
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1243	75.7	330	1	GHHU	Ig gamma-1 chain C
2	1237.5	75.3	374	2	S69339	Ig heavy chain V r
3	1237	75.3	255	4	S31866	Ig gamma-1 chain C
4	1186	72.2	234	2	PT0207	Ig gamma chain C r
5	1163	70.8	377	2	A23511	Ig gamma-3 chain C
6	1161	70.7	377	2	A60764	Ig gamma-3 chain C
7	1153	70.2	326	1	G2HU	Ig gamma-2 chain C
8	1142	69.5	327	1	G4HU	Ig gamma-4 chain C
9	1138.5	69.3	289	1	G3HUWI	Ig gamma-3 heavy c
10	934.5	56.9	323	1	GHRB	Ig gamma chain C r
11	918.5	55.9	328	2	I47159	Ig gamma 2a chain
12	917	55.8	328	2	I47160	Ig gamma 2b chain
13	915	55.7	277	2	I47162	Ig gamma 4 chain c

14	903.5	55.0	329	1	G2GP	Ig gamma-2 chain C
15	898.5	54.7	328	2	I47158	Ig gamma 1 chain c
16	891.5	54.3	328	2	I47161	Ig gamma 3 chain c
17	870.5	53.0	470	2	S22080	Ig heavy chain pre
18	856	52.1	329	1	G3MSC	Ig gamma-3 chain C
19	854	52.0	308	2	C30554	Ig heavy chain C r
20	854	52.0	472	2	S31459	Ig gamma-1 chain -
21	849	51.7	333	2	PS0018	Ig gamma-2b chain
22	845	51.4	398	1	G3MSM	Ig gamma-3 chain C
23	836.5	50.9	444	2	PC4436	monoclonal antibod
24	827	50.3	326	2	PS0017	Ig gamma-1 chain C
25	826	50.3	329	2	S00847	Ig gamma-2c chain
26	825.5	50.2	324	1	G1MS	Ig gamma-1 chain C
27	820.5	49.9	393	1	G1MSM	Ig gamma-1 chain C
28	819.5	49.9	330	1	G2MSA	Ig gamma-2a chain
29	819.5	49.9	469	2	S37483	Ig gamma-2a chain
30	818.5	49.8	335	1	G2MSAB	Ig gamma-2a chain
31	814.5	49.6	399	1	G2MSAM	Ig gamma-2a chain
32	804.5	49.0	446	2	S40295	Ig gamma-2a chain
33	796	48.4	322	2	PS0019	Ig gamma-2a chain
34	792	48.2	474	1	G2MS11	Ig gamma-2b chain
35	785	47.8	327	2	S06611	Ig gamma-2 chain C
36	784.5	47.7	405	1	G2MSBM	Ig gamma-2b chain
37	767.5	46.7	475	2	S01321	Ig gamma-2b chain
38	707	43.0	180	2	I46732	Ig gamma heavy cha
39	577.5	35.1	249	2	S69340	Ig heavy chain VHI
40	574.5	35.0	218	2	A36040	Ig heavy chain V-I
41	571	34.8	152	2	S14236	Ig gamma-1 chain C
42	400	24.3	572	2	B46529	Ig Y heavy chain (
43	364.5	22.2	549	2	S04845	Ig heavy chain pre
44	362.5	22.1	388	1	EHMS	Ig epsilon chain C
45	359.5	21.9	548	2	S38864	Ig epsilon chain C

ALIGNMENTS

RESULT 1

GHHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, 239-Asp and 241-Leu

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861
 A;Molecule type: DNA
 A;Residues: 2-330 <HAR>
 A;Cross-references: EMBL:Z17370
 R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982
 A;Title: Structure of human immunoglobulin gamma genes: implications for
 evolution of a gene family.
 A;Reference number: S33887; MUID:83001943; PMID:6811139
 A;Accession: S33887
 A;Molecule type: DNA
 A;Residues: 88-113;235-330 <TAK>
 A;Cross-references: EMBL:Z17370
 R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.;
 Edelman, G.M.
 Biochemistry 9, 3161-3170, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino
 acid sequence of heavy-chain cyanogen bromide fragments H-1-H-4.
 A;Reference number: A90563; MUID:71064024; PMID:5489771
 A;Contents: myeloma protein Eu
 A;Accession: B90563
 A;Molecule type: protein
 A;Residues: 1-96,'R',98-135 <CUN>
 A;Note: this sequence has the Glm(3) marker, 97-Arg
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman,
 G.M.
 Biochemistry 9, 3171-3181, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino
 acid sequence of heavy-chain cyanogen bromide fragments H-5-H-7.
 A;Reference number: A90564; MUID:71064025; PMID:5530842
 A;Contents: Eu
 A;Accession: A90564
 A;Molecule type: protein
 A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-
 238,'E',240,'M',242-267,'DGEPE',273-329 <RUT>
 A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
 R;Ponstingl, H.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
 (Myelomprotein Nie), III. Die chymotryptischen Peptide der H-Kette, Anordnung
 der tryptischen Peptide und Diskussion der vollstaendigen Primaerstruktur.
 A;Reference number: A91668; MUID:77070269; PMID:826475
 A;Contents: myeloma protein Nie
 A;Accession: B91668
 A;Molecule type: protein
 A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-
 268,'E',270-271,'D',273-330 <PON>
 A;Note: this sequence has the Glm(17) and Glm(1) markers
 R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
 A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins
 IgG1 KOL, I.
 A;Reference number: A91723; MUID:83289131; PMID:6884994
 A;Contents: myeloma protein KOL; disulfide bonds
 A;Accession: A91723
 A;Molecule type: protein

|||||
Db 317 NHYTQKSLSLSPGK 330

RESULT 2

S69339

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C;Accession: S69339; S72664

R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A;Reference number: S69339; MUID:95262687; PMID:7744049

A;Accession: S69339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <KHA>

A;Cross-references: EMBL:X81695

R;Khamlichi, A.A.

submitted to the EMBL Data Library, September 1994

A;Reference number: S72664

A;Accession: S72664

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140,'C',142-374 <KH2>

A;Cross-references: EMBL:X81695

C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 75.3%; Score 1237.5; DB 2; Length 374;
Best Local Similarity 79.0%; Pred. No. 2.5e-82;
Matches 237; Conservative 9; Mismatches 23; Indels 31; Gaps 2;

```
Qy      23 TMLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNAS----- 67
      | | : | : | | : | | | |
Db      86 TRLTITKDTSKNQVV-----LTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQ 134

Qy      68 -----VTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 122
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     135 GTLVTVSSEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 194

Qy     123 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     195 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 254

Qy     183 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 242
      | | | | | | | | | | | | | | | | : | : | | | | | | | | | | | |
Db     255 LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP 314

Qy     243 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 302
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     315 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 374
```

RESULT 3

S31866

Query Match 72.2%; Score 1186; DB 2; Length 234;

Best Local Similarity 94.8%; Pred. No. 7.8e-79;
Matches 221; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

[illegible]

RESULT 5

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 23-Jul-1999

C;Accession: A23511

R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A7>Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region
gene: comparison with the other human C-gamma genes.

A;Reference number: A23511; MUJID:86148507; PMID:3081877

A;Accession: A23511

A;Molecule type: DNA

A;Residues: 1-377 <HUC>

A;Cross-references: GB:X03604; GB:M12958; NID:q33070; PIDN:CAA27268.1;

PID:q577056

C; Genetics:

A;Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

```
A;Map position: 14q32.33-14q32.33
```

A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 1163; DB 2; Length 377;
Best Local Similarity 84.7%; Pred. No. 6.4e-77;
Matches 221; Conservative 9; Mismatches 19; Indels 12; Gaps 4;

```
Qy      46 PCQLRC----SSNTPPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPK 101
        || ||   | :|||  ||              | |   || ||||| ||||| |||||
Db     125 PCP-RCPEPKSCDTPP-PCPR-----CPEPKSCDTPPPCRPAPELLGGPSVFLFPPK 176

Qy     102 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 161
        ||||| ||||| ||||| ||||| ||||| :| ||||| ||||| ||||| ||||| :|||
Db     177 PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVL 236
```


RESULT 7

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.

A;Reference number: A92809; MUID:81007873; PMID:6774012

A;Contents: myeloma protein Til

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Contents: myeloma protein Zie

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-234,'Z',236-263,'BGEpz',269-325 <CON>

A;Note: this sequence has since been revised

R;Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.

A;Reference number: A93132; MUID:80114419; PMID:118920

A;Contents: Zie

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Reference number: A94591

A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidation states of residues 58, 194, and 197; the amidation states of residues 172-174, 176, and 235 were not determined

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.2%; Score 1153; DB 1; Length 326;
Best Local Similarity 87.6%; Pred. No. 2.8e-76;
Matches 218; Conservative 8; Mismatches 15; Indels 8; Gaps 3;

```

Qy      61 QRY-CNASVTNSVKGVDKT-----HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPE 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      79 QTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPE 137

Qy     114 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 173
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     138 VTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKE 197

Qy     174 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 233
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     198 YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA 257

Qy     234 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQ 293
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     258 VEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQ 317

Qy     294 KSLSLSPGK 302
      | | | | | | | |
Db     318 KSLSLSPGK 326

```

RESULT 8

G4HU

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C;Accession: A90933; A90249; A02150

QY 290 HYTQKSLSLSPGK 302

Db

||||||| ||
315 HYTQKSLSLSLGK 327

RESULT 9

G3HUWI

Ig gamma-3 heavy chain disease proteins - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999

C;Accession: A90442; A92219; A90198; A93915; A02149

R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein Wis.

A;Reference number: A90442; MUID:81021548; PMID:6774747

A;Contents: heavy chain disease protein Wis

A;Accession: A90442

A;Molecule type: protein

A;Residues: 1-289 <FRA>

A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain disulfide bond at position 7 in addition to the 11 normally present in the hinge region

A;Note: this protein lacks most of the V region and all of the CH1 region.

Residue 12 corresponds to the beginning of the hinge region of normal gamma-3 chains

A;Note: the sequence of residues 42-76 was taken from the reference that follows

R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.

A;Reference number: A92219; MUID:77118561; PMID:402363

A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein Wis

A;Accession: A92219

A;Molecule type: protein

A;Residues: 12-97 <MIC>

A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical 15-residue segments (29-43, 44-58, and 59-73) preceded by a similar 17-residue segment (12-28)

A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter-heavy chain bonds

R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.

Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the Fc fragment of immunoglobulin G3.

A;Reference number: A90198; MUID:77021516; PMID:823945

A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues 59-289 of protein Wis

A;Accession: A90198

A;Molecule type: protein

A;Residues: 59-125,'EB',128-226,228-289 <WOL>

A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the hinge compared with normal gamma-3 heavy chains

R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Buxbaum, J.N.

Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982

A;Reference number: A91749; MUID:84030930; PMID:6313520
 A;Accession: A91749
 A;Molecule type: mRNA
 A;Residues: 1-323 <BER>
 A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
 R;Pratt, D.M.; Mole, L.E.
 Biochem. J. 151, 337-349, 1975
 A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.
 A;Reference number: A90290; MUID:76135469; PMID:1243651
 A;Accession: A90290
 A;Molecule type: protein
 A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
 R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain and identification of two genomic C-gamma genes.
 A;Reference number: A93928; MUID:83299917; PMID:6193512
 A;Accession: A93928
 A;Molecule type: mRNA
 A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
 A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
 A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala
 R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
 Biochem. J. 116, 249-259, 1970
 A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.
 A;Reference number: A90245; MUID:70110015; PMID:5461106
 A;Accession: A90245
 A;Molecule type: protein
 A;Residues: 132-143,'E',145-161 <FRU>
 R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
 in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, Stockholm, 1967
 A;Reference number: A94416
 A;Accession: A94416
 A;Molecule type: protein
 A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',234-245,'D',247-255,'G',257-259,'D',261-265,'D',267-279,'W',281-283,'S',285-322 <HIL>
 A;Note: this has the e15 allotypic marker, 185-Ala
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-82/Domain: immunoglobulin homology <IM1>
 F;130-199/Domain: immunoglobulin homology <IM2>
 F;236-303/Domain: immunoglobulin homology <IM3>
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 934.5; DB 1; Length 323;
 Best Local Similarity 68.0%; Pred. No. 1.9e-60;
 Matches 174; Conservative 33; Mismatches 40; Indels 9; Gaps 3;

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Qy      22 VTMLQMAGQCSONEY-FDSSLHACIPQLRCSN--TTP---LTCQRY-CNASVTNSVKG   74  
       || : | | : | |:| | | : | | : : | || :  
Db     37 VTVTWNSGALSSGVHTFPSVLQ---PSGLYSLSSMVTVPASSLSKSYTCNVNHPPATTTK 93  
  
Qy     75 VDK---THTCPPECP-----APELLGGPSVFLFPPPKP KDTLMISRTPEVTCVVVDVSHED 125  
       ||| | | |||| :| |||||:|||||:|||||:|||||:|||||:  
Db    94 VDKRVGTGTKPPCPI CPACESP----GPSVFIFPPPKP KDTLMISRTPQVTCVVVDVSQEN 149  
  
Qy    126 PEVKFNWYVDGEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYCKVSNKALPA 185  
       |||:||||| |||::|::|::|::|::|::|::|::|::|::|::|::|::|
```

Db 150 PEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPA 209
 Qy 186 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PE 243
 || : ||||| ||||| :||::||:| || | ||: || ||
 Db 210 PITRIISKAKGQTREPQVYTLPPHAEELSRKVSITCLVIGFYPPDIDVEWQRNGQPEPE 269
 Qy 244 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
 ||:|||| | ||:|||| :||: || | :| :|||||||:| :||
 Db 270 GNYRTTPPQQDVGTYFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

RESULT 12

I47160

Ig gamma 2b chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: I47160

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47160

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126

C;Genetics:

A;Gene: IgG2b

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 55.8%; Score 917; DB 2; Length 328;

Best Local Similarity 66.9%; Pred. No. 3.6e-59;

Matches 172; Conservative 34; Mismatches 35; Indels 16; Gaps 5;

Qy 58 LTCQRY-CNASVTNSVKGVDK---THTCPPCP-----APELLGGPSVFLFPPKPKDTLM 107
 |: : | | : : || | | | :| ||||:|||||||
 Db 76 LSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----GPSVFIFPPKPKDTLM 131
 Qy 108 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD 167
 ||||:||||||| |:|:|:| ||||| |:|:|:|:| ||||| : |||
 Db 132 ISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHGD 191
 Qy 168 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF 227
 |||||:||||:| ||||| : ||||| ||||| :||::||:| || ||
 Db 192 WLNGKEFKCKVNNKDLAPITRIISKAKGQTREPQVYTLPPHAEELSRKVSITCLVIGF 251
 Qy 228 YPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 285
 || || ||: || || |:| || | ||:| || | ||: || | :| ||||
 Db 252 YPPDIDVEWQRNGQPEPEGNYRTTPPQQDVGTYFLYSKFSVDKASWQGGGIFQCAVMHE 311
 Qy 286 ALHNHYTQKSLSLSPGK 302
 ||||| ||||:| :|||
 Db 312 ALHNHYTQKSISKTPGK 328

I47162

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: I47162

J. Immunol. 153, 3565-3573, 1994

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-277 <KAC>

C;Genetics:

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 915; DB 2; Length 277;
Best Local Similarity 68.0%; Pred. No. 4.1e-59;
Matches 172; Conservative 33; Mismatches 40; Indels 8; Gaps 5;

Db 25 LSSKSYTCNVNHPATTTKVDRVGTGTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRT 84

Db 85 PKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNG 144

Db 145 KEFKCKVNNKDLPAITRIISKAKGQTREPQVYTLPPPTTEELSRSKVTLTCLVTGFYPPD 204

Db 205 IDVEWQRNGQPEPEGNYRTPPQQDVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHN 264

Db 265 HYTQKSIKTPGK 277

G2GP

C;Species: Cavia porcellus (guinea pig)

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151

submitted to the Atlas, April 1975

A;Accession: A94553

A;Molecule type: protein

A;Residues: 1-3 <TRI>
 R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
 Biochemistry 10, 18-25, 1971
 A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).
 III. Amino acid sequence of the region around the half-cystine joining heavy and
 light chains.
 A;Reference number: A90352; MUID:71058471; PMID:5538606
 A;Accession: A90352
 A;Molecule type: protein
 A;Residues: 4-68 <BIR>
 R;Turner, K.J.; Cebra, J.J.
 Biochemistry 10, 9-17, 1971
 A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).
 II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen
 bromide fragments.
 A;Reference number: A90359; MUID:71058486; PMID:5538616
 A;Accession: A90359
 A;Molecule type: protein
 A;Residues: 69-133;312-329 <TUR>
 R;Tracey, D.E.; Cebra, J.J.
 Biochemistry 13, 4796-4803, 1974
 A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2
 antibodies.
 A;Reference number: A90384; MUID:75036072; PMID:4429665
 A;Accession: A90384
 A;Molecule type: protein
 A;Residues: 134-226 <TRA>
 R;Trischmann, T.M.; Cebra, J.J.
 Biochemistry 13, 4804-4811, 1974
 A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2
 antibodies.
 A;Reference number: A90385; MUID:75036073; PMID:4609467
 A;Accession: A90385
 A;Molecule type: protein
 A;Residues: 227-311 <TR2>
 R;Oliveira, B.; Lamm, M.E.
 Biochemistry 10, 26-31, 1971
 A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
 A;Reference number: A90354; MUID:71058474; PMID:4922544
 A;Contents: annotation; disulfide bonds
 A;Note: Cys-16 is involved in a heavy-light chain bond
 A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
 C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea
 pigs.
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical
 light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma,
 or mu) chains usually stabilized by interchain disulfide bonds. In some cases,
 such as IgA and IgM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;21-81/Domain: immunoglobulin homology <IM1>
 F;135-204/Domain: immunoglobulin homology <IM2>
 F;241-310/Domain: immunoglobulin homology <IM3>
 F;28-79/Disulfide bonds: #status experimental
 F;142-202/Disulfide bonds: #status experimental
 F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;248-308/Disulfide bonds: #status experimental

Query Match 55.0%; Score 903.5; DB 1; Length 329;
Best Local Similarity 65.8%; Pred. No. 3.4e-58;
Matches 171; Conservative 27; Mismatches 49; Indels 13; Gaps 2;

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Qy      55 TPPLTCQRYCNASVTSVKGVDKT-----HTCPPCPAPELLGGPSVFLFPPKPK 103
      | | : : | | : | ||| || | | |||||:|||||
Db      70 TVPSSQKATCNVAHPASSTKVDKTVEPIRTPZPBPCCTCPKCPPPENLGGPSVFI FPPKPK 129

Qy     104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
      ||||| || ||||| ||| :|||:| |:|| | ||:|||| ||||:|:|| ||| :
Db     130 DTLMISLTPRVTCVVVDVSQDEPEVQFTWTFVDNKPVGNAETKPRVEQYNTTFRVESVLPI 189

Qy     164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
      ||||| |||:|||| ||||| ||||| || || | ||||| ||||:|:||:||||
Db     190 QHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCL 249

Qy     224 VKGFYPSDIAVEWESNGQP--ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVSCS 281
      : |:|| || || || | | |||: |:||:||||||| || || |:|||
Db     250 IINFFPADIHVEWASNRVPVSEKEYKNTPIEDADGSYFLYSKLTVDKSAWDQGTVYTCS 309

Qy     282 VMHEALHNHYTQKSLSLSPG 301
      ||||| |||:| |||
Db     310 VMHEALHNHVTQKAISRSPG 329
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RESULT 15

I47158

Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: I47158

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47158

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122

C;Genetics:

A;Gene: IgG1

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 54.7%; Score 898.5; DB 2; Length 328;
Best Local Similarity 59.6%; Pred. No. 7.8e-58;
Matches 180; Conservative 39; Mismatches 64; Indels 19; Gaps 7;

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Qy      10 VLLLVWPGS-TGDV---TMLQMGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYC 64
      | : | |: | | :||:| | : | | :| | :|
Db      37 VTVTWNSGALTSGVHTFPSVLQPSGLYSLSSM-----VTVPAS---SLSSKSYTCNVNH 87

Qy     65 NASVTNSVK--GVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 122
      |: | | |: : ||| || | : ||||:||||||| ||||| |||||
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Db 88 PATTTKVDKRVGIHQPTCPICPGCE-VAGPSVFIFPPKPKDTLMISQTPEVTCVWVDVS 146
 Qy 123 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 182
 | ||:||||| ||:||||:||||| : |||| ||:||||:|
 Db 147 KEHAEVQFSWYVDGVEVHTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVD 206
 Qy 183 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ- 241
 |||| :|||| || ||||| :||:||||:|||| |||| || ||:||||
 Db 207 LPAPITRTISKAIGQSREPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQP 266
 Qy 242 -PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 300
 ||| |:|||| | ||:||||| ||:| |: | |:|||||:| :
 Db 267 EPENTYRTTPPQQDVGDTFFLYSKLAVDKARWDHGDKFECAMHEALHNHYTQKSISKTK 326
 Qy 301 GK 302
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 Db 327 GK 328

Search completed: April 19, 2004, 13:23:36
 Job time : 17.7778 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:21:03 ; Search time 47.2263 Seconds
(without alignments)
1762.857 Million cell updates/sec

Title: PCT-US03-05147-3
Perfect score: 1643
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1643	100.0	302	14	US-10-115-192-12	Sequence 12, Appl
2	1488.5	90.6	283	9	US-09-854-864-9	Sequence 9, Appli
3	1488.5	90.6	283	12	US-09-855-158-9	Sequence 9, Appli
4	1398.5	85.1	281	9	US-09-854-864-10	Sequence 10, Appl
5	1398.5	85.1	281	12	US-09-855-158-10	Sequence 10, Appl
6	1379	83.9	334	15	US-10-258-368-8	Sequence 8, Appli
7	1376	83.7	366	15	US-10-258-368-6	Sequence 6, Appli
8	1361	82.8	320	12	US-10-411-037-50	Sequence 50, Appl
9	1361	82.8	320	12	US-10-411-026-50	Sequence 50, Appl
10	1276.5	77.7	396	14	US-10-193-616-14	Sequence 14, Appl
11	1271	77.4	332	14	US-10-152-363A-62	Sequence 62, Appl
12	1269	77.2	446	9	US-09-792-200B-10	Sequence 10, Appl
13	1265.5	77.0	465	9	US-09-792-200B-6	Sequence 6, Appli
14	1264.5	77.0	398	15	US-10-622-407-14	Sequence 14, Appl
15	1264.5	77.0	404	15	US-10-258-368-15	Sequence 15, Appl
16	1263	76.9	348	14	US-10-152-363A-54	Sequence 54, Appl
17	1260	76.7	608	14	US-10-363-427-10	Sequence 10, Appl
18	1259.5	76.7	397	9	US-09-854-864-18	Sequence 18, Appl
19	1259.5	76.7	397	12	US-09-855-158-18	Sequence 18, Appl
20	1259	76.6	480	14	US-10-077-023-133	Sequence 133, App
21	1259	76.6	480	14	US-10-077-023-135	Sequence 135, App
22	1259	76.6	698	9	US-09-875-338-9	Sequence 9, Appli
23	1259	76.6	698	14	US-10-077-023-9	Sequence 9, Appli
24	1258	76.6	344	14	US-10-152-363A-52	Sequence 52, Appl
25	1257.5	76.5	360	9	US-09-949-713-11	Sequence 11, Appl
26	1257.5	76.5	376	9	US-09-949-713-22	Sequence 22, Appl
27	1257.5	76.5	376	14	US-10-084-139-10	Sequence 10, Appl
28	1254	76.3	266	15	US-10-390-566-21	Sequence 21, Appl
29	1254	76.3	266	15	US-10-390-566-28	Sequence 28, Appl
30	1254	76.3	494	9	US-09-792-200B-2	Sequence 2, Appli
31	1253.5	76.3	357	14	US-10-152-363A-56	Sequence 56, Appl
32	1252	76.2	266	15	US-10-390-566-8	Sequence 8, Appli
33	1252	76.2	266	15	US-10-390-566-15	Sequence 15, Appl
34	1252	76.2	444	14	US-10-363-427-2	Sequence 2, Appli
35	1252	76.2	628	14	US-10-363-427-6	Sequence 6, Appli
36	1251.5	76.2	523	9	US-09-792-200B-14	Sequence 14, Appl
37	1251	76.1	400	10	US-09-389-782-5	Sequence 5, Appli
38	1250.5	76.1	387	12	US-10-050-227-4	Sequence 4, Appli
39	1249	76.0	252	14	US-10-145-206-121	Sequence 121, App
40	1249	76.0	528	9	US-09-792-200B-22	Sequence 22, Appl
41	1248.5	76.0	535	12	US-10-633-202-3	Sequence 3, Appli
42	1248	76.0	288	10	US-09-822-851B-14	Sequence 14, Appl
43	1248	76.0	288	14	US-10-119-637A-14	Sequence 14, Appl
44	1248	76.0	358	14	US-10-233-150-5	Sequence 5, Appli
45	1247	75.9	380	9	US-09-948-018-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
 US-10-115-192-12
 ; Sequence 12, Application US/10115192
 ; Publication No. US20030082175A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Apotech R & D S.A.

```
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12
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Query Match          100.0%; Score 1643; DB 14; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 METDTLLLWVLLLWVPGSTGDVTMLQMAGQCSQNEYFDSLLHACIPCQLRCSNTPPLTC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 METDTLLLWVLLLWVPGSTGDVTMLQMAGQCSQNEYFDSLLHACIPCQLRCSNTPPLTC 60

Qy     61 QRYCNASVTNSVKGVDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QRYCNASVTNSVKGVDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD 120

Qy    121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180

Qy    181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240

Qy    241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 300

Qy     301 GK 302
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Db     301 GK 302
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RESULT 2

US-09-854-864-9

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; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA,
```

```
; TITLE OF INVENTION:  BLYS/AGP-3, AND TACI
; FILE REFERENCE:  A-686B
; CURRENT APPLICATION NUMBER:  US/09/854,864
; CURRENT FILING DATE:  2001-09-11
; PRIOR APPLICATION NUMBER:  US 60/204,039
; PRIOR FILING DATE:  2000-05-12
; PRIOR APPLICATION NUMBER:  US 60/214,591
; PRIOR FILING DATE:  2000-06-27
; NUMBER OF SEQ ID NOS:  31
; SOFTWARE:  PatentIn version 3.1
; SEQ ID NO 9
; LENGTH:  283
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-854-864-9
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Query Match          90.6%;  Score 1488.5;  DB 9;  Length 283;
Best Local Similarity  97.2%;  Pred. No. 4.6e-113;
Matches  275;  Conservative  0;  Mismatches  1;  Indels  7;  Gaps  1;
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Qy      27  MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
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Qy      80  TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139
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Db      61  TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 120

Qy     140  HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199
          |||
Db     121  HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 180

Qy     200  EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
          |||
Db     181  EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 240

Qy     260  FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
          |||
Db     241  FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 283
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RESULT 3

US-09-855-158-9

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; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT:  THEILL, LARS EYDE
; APPLICANT:  YU, GANG
; TITLE OF INVENTION:  METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA, BLYS/AGP-
; TITLE OF INVENTION:  3, AND TACI
; FILE REFERENCE:  A-686A
; CURRENT APPLICATION NUMBER:  US/09/855,158
; CURRENT FILING DATE:  2001-09-11
; PRIOR APPLICATION NUMBER:  US 60/214,591
; PRIOR FILING DATE:  2000-06-27
; PRIOR APPLICATION NUMBER:  US 60/204,039
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; PRIOR FILING DATE: 2000-05-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-855-158-9

Query Match 90.6%; Score 1488.5; DB 12; Length 283;
 Best Local Similarity 97.2%; Pred. No. 4.6e-113;
 Matches 275; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

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Qy	80	TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	139
Db	61	TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	120
Qy	140	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	199
Db	121	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	180
Qy	200	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF	259
Db	181	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF	240
Qy	260	FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	302
Db	241	FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	283

RESULT 4

US-09-854-864-10
 ; Sequence 10, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Mus musculus

US-09-854-864-10

Query Match 85.1%; Score 1398.5; DB 9; Length 281;
Best Local Similarity 92.2%; Pred. No. 9.7e-106;
Matches 261; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

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Qy      80 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139
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Qy     140 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199
      |||||||||||||||||||||||||||||||||||||||||||||||
Db     119 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 178

Qy     200 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
      |||||||||||||||||||||||||||||||||||||||||||||||
Db     179 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 238

Qy     260 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 302
      |||||||||||||||||||||||||||||||||||||||||||||||
Db     239 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 281
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RESULT 5

US-09-855-158-10

; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA, BLYS/AGP-
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match 85.1%; Score 1398.5; DB 12; Length 281;
Best Local Similarity 92.2%; Pred. No. 9.7e-106;
Matches 261; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

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Qy      27 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
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Db      1 METDTLLLWVLLLLWVPGSTGDVR-----SCPEEQYWDPLLGTCMSCKTICNHQSQRCA 54

Qy     57 -----PLTCQRYCNASVTNSVK-GVDKTHTCP 82
          | | : | : : | | | | | | 
Db     55 AFCRSLSCRKEQGKFYDHLLRDCISCASICGHQHPKCAYFCENKLRSVPNLPVDKTHTCP 114

Qy     83 PCPAPELLGGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 142
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```


Qy 177 KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 236
 |||||||
 Db 241 KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 300
 Qy 237 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSL 296
 |||||||
 Db 301 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSL 360
 Qy 297 SLSPGK 302
 |||||
 Db 361 SLSPGK 366

RESULT 8

US-10-411-037-50
 ; Sequence 50, Application US/10411037
 ; Publication No. US20040043446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: DeFrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bowe, Caryn
 ; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF
 ALPHA
 ; TITLE OF INVENTION: GALACTOSIDASE A
 ; FILE REFERENCE: 040853-01-5082
 ; CURRENT APPLICATION NUMBER: US/10/411,037
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 50
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-411-037-50

Query Match 82.8%; Score 1361; DB 12; Length 320;
 Best Local Similarity 82.2%; Pred. No. 1.3e-102;
 Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

QY 1 METDTLLLWVLLLWVPGSTGDVTM--LQMAQ-----CSQNEYFDSLLHACIPCQL-- 49
 ||||| : | | | : | |
 Db 1 METDTLLLWVLLLWVPGSTGDVRRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLR 60

QY 50 -----RCSSNTPPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPPELLGGPSVFLFPPKP 102
 || | : |||||
 Db 61 TPRPKPAGASSPAPRTALQPQESVGAGAGEAAVDKTHTCPPCPAPPELLGGPSVFLFPPKP 120

QY 103 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 162
 |||||
 Db 121 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 180

QY 163 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 222
 |||||
 Db 181 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 240

QY 223 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 282
 |||||
 Db 241 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 300

QY 283 MHEALHNHYTQKSLSLSPGK 302
 |||||
 Db 301 MHEALHNHYTQKSLSLSPGK 320

RESULT 9

US-10-411-026-50

; Sequence 50, Application US/10411026

; Publication No. US20040063911A1

; GENERAL INFORMATION:

; APPLICANT: Neose Technologies, Inc.

; APPLICANT: DeFrees, Shawn

; APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David

; APPLICANT: Chen, Xi

; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

; TITLE OF INVENTION: METHODS

; FILE REFERENCE: 040853-01-5053

; CURRENT APPLICATION NUMBER: US/10/411,026

; CURRENT FILING DATE: 2003-04-09

; PRIOR APPLICATION NUMBER: US 60/328,523

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/344,692

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/391,777

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: US 60/396,594

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/404,249

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 50
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-411-026-50

Query Match 82.8%; Score 1361; DB 12; Length 320;
 Best Local Similarity 82.2%; Pred. No. 1.3e-102;
 Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

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Qy      1 METDTLLLWVLLLWVPGSTGDVTM--LQMAQ-----CSQNEYFDSLLHACIPCQL-- 49
      |||||||||||||||||||:|:| |||:|:|
Db      1 METDTLLLWVLLLWVPGSTGDVRRGPRSLRGRDAPAPTPCVPAPAECDLLVRHCVACGLLR 60

Qy     50 -----RCSSNTPPLTCQRYCNASVTNSVKGVDKHTHTCPPCPAPPELLGGPSVFLFPPKP 102
      || | | : |||||||||||||||||||
Db     61 TPRPKPAGASSAPRTALQPQESVGAGAGEAAVDKHTHTCPPCPAPPELLGGPSVFLFPPKP 120

Qy    103 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 162
      |||||||||||||||||||
Db    121 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 180

Qy    163 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 222
      |||||||||||||||||||
Db    181 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 240

Qy    223 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV 282
      |||||||||||||||||||
Db    241 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV 300

Qy    283 MHEALHNHYTQKSLSLSPGK 302
      |||||||
Db    301 MHEALHNHYTQKSLSLSPGK 320
  
```

RESULT 10

US-10-193-616-14

; Sequence 14, Application US/10193616

; Publication No. US20030096355A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Ke

; TITLE OF INVENTION: Isolation, Identification, and Characterization of

; TITLE OF INVENTION: ymkz5, a novel

; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family

; FILE REFERENCE: 01017/35551A

; CURRENT APPLICATION NUMBER: US/10/193,616

; CURRENT FILING DATE: 2002-07-11

; PRIOR APPLICATION NUMBER: US/09/611,989

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,137

; PRIOR FILING DATE: 1999-07-07

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 396

; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymkz5-Fc fusion protein
US-10-193-616-14

Query Match 77.7%; Score 1276.5; DB 14; Length 396;
Best Local Similarity 82.4%; Pred. No. 1.3e-95;
Matches 244; Conservative 7; Mismatches 24; Indels 21; Gaps 5;

```
Qy      27 MAGQCSQNE-----YFD-SLLHACIPCQLRCSSNTPPL-----TCQRYCNASVT 69
      |  ||                |:|      :| || :|      | |      |  ||::||:
Db      102 MVADCSATSDRKCECQIGLYYYDPKFPESCRPC-TKCPQGIPVLQECNSTANTVCSSSVS 160

Qy      70 NSV---KGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 126
      |:  |  |||||||||||||||||||||||||||||||||||||||||||||
Db      161 NAAAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 220

Qy     127 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 186
      |||||||||||||||||||||||||||||||||||||||||||||
Db     221 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 280

Qy     187 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 246
      |||||||||||||||||||||||||||||||||||||||||||||
Db     281 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 340

Qy     247 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
      |||||||||||||||||||||||||||||||||||||||||||||
Db     341 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 396
```

RESULT 11

US-10-152-363A-62
; Sequence 62, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein.
US-10-152-363A-62

Query Match 77.4%; Score 1271; DB 14; Length 332;
Best Local Similarity 72.2%; Pred. No. 2.9e-95;
Matches 239; Conservative 15; Mismatches 37; Indels 40; Gaps 2;


```

Qy      9 WVLLWVPGSTGDVTMLQMGQCSQNEYFDSLLHACIPCQLRCSSNTP----- 56
      |: | : |: | :|      | : |:| || |: |: |: :
Db      5 WIFLFLSGTAG---VLSAMRSCPEEQYWDPLLGTMSCKTICNHQSQRTCAAFCSRSLSC 61

Qy      57 -----PLTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLG 91
      | | :| : : | |||||
Db      62 RKEQGKFYDHLLRDCISCASICGQHPKQCAIFCENKLRSEPKSSDKTHTCPPCPAPEAEG 121

Qy      92 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 151
      |||||
Db      122 APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 181

Qy      152 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 211
      |||||: |||||
Db      182 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSRD 241

Qy      212 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 271
      |||||
Db      242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 301

Qy      272 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
      |||||
Db      302 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332

```

RESULT 12

```

US-09-792-200B-10
; Sequence 10, Application US/09792200B
; Patent No. US20020042368A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Fanslow, William C.
; APPLICANT: Poindexter, Kurt
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: INTEGRIN ANTAGONISTS
; FILE REFERENCE: 2958-A
; CURRENT APPLICATION NUMBER: US/09/792,200B
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/184,865
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-792-200B-10

```

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Query Match          77.2%; Score 1269; DB 9; Length 446;
Best Local Similarity 57.2%; Pred. No. 6e-95;
Matches 261; Conservative 2; Mismatches 29; Indels 164; Gaps 5;

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Qy      1 METDTLLWVLLWVPGSTG-----DVTMLQMGQC 31

```

Db	1		1	METDTLLLWVLLLVPGSTGTSCGNSRVDEGEEDPGIMYLNNDTCCNSDCT-LKEGVQC	59
Qy	32	SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNAS-----			67
Db	60	SDRN-----SPCCKNCQFETAQKKCQEA	INATCKGVSYCTGNSSECPPPGNAEDDT		110
Qy	68	-----VTNSVK-----			73
Db	111	VCLDLGKCKDGKCI	PFCEREQQLESCACNETDNSCKVCCRDLSGRCVPYVDAEQKNLFLR		170
Qy	74	-----GVDKTHTCPPCPA			86
Db	171	KGKPC'TVGFCDMNGKCEKRVQDVIERFWDFIDQLSINTFGKFLADNRSCDKTHTCPPCPA			230
Qy	87	PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP			146
Db	231	PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP			290
Qy	147	REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL			206
Db	291	REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL			350
Qy	207	PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT			266
Db	351	PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT			410
Qy	267	VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK			302
Db	411	VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK			446

RESULT 13

US-09-792-200B-6

```
; Sequence 6, Application US/09792200B
; Patent No. US20020042368A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Fanslow, William C.
; APPLICANT: Poindexter, Kurt
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: INTEGRIN ANTAGONISTS
; FILE REFERENCE: 2958-A
; CURRENT APPLICATION NUMBER: US/09/792,200B
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/184,865
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-792-200B-6
```

Query Match 77.0%; Score 1265.5; DB 9; Length 465;
 Best Local Similarity 56.1%; Pred. No. 1.2e-94;
 Matches 261; Conservative 11; Mismatches 30; Indels 163; Gaps 7;

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Qy      1 METDTLLLWVLLLWVPGSTG-----DVTM-----L 25
      |||
Db      1 METDTLLLWVLLLWVPGSTGTSCGNGMVEQGEECDGCGYSDQCKDECCFDANQPEGRKCKL 60

Qy     26 QMAGQCSQNE-----YFDSLLHACIP----- 46
      : ||| :: | : | |
Db     61 KPGKQCSQSPQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALCPASDPKPNFTDCNR 120

Qy     47 -----CQLRCSSNTPPLTC----- 60
      | : | | |
Db    121 HTQVCINGQCAGSICEKYGLEECTCASSDGKDDKELCHVCCMKMDPSTCASTGSGVQWSR 180

Qy     61 -----QRYCN-----ASVTNSV-----KGVDK 77
      : ||: | : :: : ||
Db    181 HFSGRITITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAI FSPELYENIAERSCDK 240

Qy     78 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 137
      |||
Db    241 THTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 300

Qy    138 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 197
      |||
Db    301 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 360

Qy    198 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 257
      |||
Db    361 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 420

Qy    258 SFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 302
      |||
Db    421 SFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 465
  
```

RESULT 14

US-10-622-407-14

; Sequence 14, Application US/10622407

; Publication No. US20040018544A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2,
 A NOVEL

; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

; FILE REFERENCE: 01017/35434B

; CURRENT APPLICATION NUMBER: US/10/622,407

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: US 09/612,033

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

```

; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-10-622-407-14

```

[illegible]

RESULT 15

```
; Sequence 15, Application US/10258368
; Publication No. US20040013674A1
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-15
```

Query Match 77.0%; Score 1264.5; DB 15; Length 404;
 Best Local Similarity 77.7%; Pred. No. 1.2e-94;
 Matches 244; Conservative 6; Mismatches 19; Indels 45; Gaps 3;

```

Qy      33 QNEYFDSLHACIPC-----QLRCSSNTPPLTCQRYCNASVTN----- 70
      |:::|| || || |          :||  ||  :| :  ||
Db      92 QGKFYDHLRDCISCASICGQHPKQCAYFCENKLRSPVNLPP-ELRRQRSGEVENNSDNS 150

Qy      71 -----SVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 108
      | |||||
Db     151 GRYQGLEHRGSEASPALPGLKLSADQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 210

Qy     109 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 168
      |||||
Db     211 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 270

Qy     169 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 228
      |||||
Db     271 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 330

Qy     229 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALH 288
      |||||
Db     331 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALH 390

Qy     289 NHYTQKSLSLSPGK 302
      |||||
Db     391 NHYTQKSLSLSPGK 404
  
```

Search completed: April 19, 2004, 13:25:48
 Job time : 48.2263 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:32 ; Search time 44.7407 Seconds
(without alignments)
2129.748 Million cell updates/sec

Title: PCT-US03-05147-3
Perfect score: 1643
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	

1	1243	75.7	469	4	Q7Z7P5	Q7z7p5 homo sapien
2	1243	75.7	470	4	Q7Z5W1	Q7z5w1 homo sapien
3	1239	75.4	482	4	Q7Z351	Q7z351 homo sapien
4	1237	75.3	679	4	Q96PQ8	Q96pq8 homo sapien
5	1163	70.8	354	4	Q86TT2	Q86tt2 homo sapien
6	1159	70.5	521	4	Q8N4Y9	Q8n4y9 homo sapien
7	1148	69.9	509	4	Q8NF17	Q8nf17 homo sapien
8	1142	69.5	473	4	Q8TC63	Q8tc63 homo sapien
9	917.5	55.8	337	6	Q95M34	Q95m34 equus cabal
10	856	52.1	470	11	Q7TMK1	Q7tmk1 mus musculu
11	841.5	51.2	469	11	Q8R3V9	Q8r3v9 mus musculu
12	837.5	51.0	463	11	Q99LC4	Q99lc4 mus musculu
13	833.5	50.7	437	11	Q9R1A4	Q9r1a4 mus musculu
14	826.5	50.3	473	11	Q9D8L4	Q9d8l4 mus musculu
15	815.5	49.6	468	11	Q99L31	Q99l31 mus musculu
16	815.5	49.6	473	11	Q99L25	Q99l25 mus musculu
17	790.5	48.1	473	11	Q91Z05	Q91z05 mus musculu
18	790.5	48.1	474	11	Q8R3H6	Q8r3h6 mus musculu
19	358	21.8	375	4	Q86TT1	Q86tt1 homo sapien
20	358	21.8	597	4	Q9BU10	Q9bul10 homo sapien
21	358	21.8	597	4	Q9BQB8	Q9bqb8 homo sapien
22	358	21.8	597	4	Q96BB9	Q96bb9 homo sapien
23	349	21.2	614	11	Q7TMT6	Q7tmt6 mus musculu
24	348	21.2	588	4	Q8WUX4	Q8wux4 homo sapien
25	348	21.2	613	4	Q96EY0	Q96ey0 homo sapien
26	348	21.2	613	4	Q8WUK1	Q8wuk1 homo sapien
27	348	21.2	614	4	Q96GA6	Q96ga6 homo sapien
28	348	21.2	618	4	Q96AA6	Q96aa6 homo sapien
29	347	21.1	613	11	Q8VCX7	Q8vcx7 mus musculu
30	316.5	19.3	587	13	Q7T0R1	Q7t0r1 xenopus lae
31	280	17.0	384	4	Q9UP60	Q9up60 homo sapien
32	280	17.0	493	4	Q8NCL6	Q8ncl6 homo sapien
33	280	17.0	494	4	Q96K68	Q96k68 homo sapien
34	280	17.0	496	4	Q96KX8	Q96kx8 homo sapien
35	277	16.9	496	4	Q96DK0	Q96dk0 homo sapien
36	277	16.9	499	4	Q8N5K4	Q8n5k4 homo sapien
37	275	16.7	497	4	Q8WY24	Q8wy24 homo sapien
38	275	16.7	500	4	Q9BRV0	Q9brv0 homo sapien
39	274	16.7	684	13	Q90544	Q90544 ginglymosto
40	273.5	16.6	478	4	Q7Z379	Q7z379 homo sapien
41	273.5	16.6	492	4	Q7Z374	Q7z374 homo sapien
42	271.5	16.5	416	4	Q9NPP6	Q9npp6 homo sapien
43	269.5	16.4	486	11	Q91Z07	Q91z07 mus musculu
44	269.5	16.4	487	11	Q99KA4	Q99ka4 mus musculu
45	268.5	16.3	426	11	Q9DCD9	Q9dcd9 mus musculu

ALIGNMENTS

RESULT 1

Q7Z7P5

ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.

AC Q7Z7P5;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Db 456 NHYTOKSLSLSPGK 469

RESULT 2

07Z5W1

SO SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

[illegible]

Db	223	CNVNHKP-----SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI	276
Qy	109	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW	168
Db	277	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW	336
Qy	169	LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY	228
Db	337	LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY	396
Qy	229	PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQOGN VFSCSV MHEALH	288
Db	397	PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQOGN VFSCSV MHEALH	456
Qy	289	NHYTQKSLSLSPGK	302
Db	457	NHYTQKSLSLSPGK	470

072351

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ID       Q7Z351          PRELIMINARY;          PRT;    482 AA.
AC       Q7Z351;
DT       01-OCT-2003 (TrEMBLrel. 25, Created)
DT       01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT       01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE       Hypothetical protein DKFZp686N02209.
GN       DKFZP686N02209.
OS       Homo sapiens (Human).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX       NCBI_TaxID=9606;
RN       [1]
RP       SEQUENCE FROM N.A.
RC       TISSUE=Human rectum tumor;
RA       Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA       Fobo G., Han M., Wiemann S.;
RL       Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR       EMBL; BX538118; CAD98026.1; -.
KW       Hypothetical protein.
SQ       SEQUENCE    482 AA;  52852 MW;  EDA75F1901D1A034 CRC64;

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[illegible]

Qy 229 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 288
 |||
 Db 409 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLH 468
 Qy 289 NHYTQKSLSLSPGK 302
 |||
 Db 469 NHYTQKSLSLSPGK 482

RESULT 4

Q96PQ8

ID Q96PQ8 PRELIMINARY; PRT; 679 AA.
 AC Q96PQ8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Factor VII active site mutant immunoconjugate.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477448; PubMed=11593034;
 RA Hu Z., Garen A.;
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
 RT cells for immunotherapy in mouse models of prostatic cancer.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu Z., Garen A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF272774; AAK58686.2; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00047; ig; 2.
 DR Pfam; PF00089; trypsin; 1.

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ID      Q86TT2                PRELIMINARY;          PRT;    354 AA.
AC      Q86TT2;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens
DE      (Human) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;

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OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Primary B-Cells;
RA      Strausberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC033178; AAH33178.1; -.
DR      PIR; A60764; A60764.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 4.
DR      SMART; SM00407; IGc1; 3.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE      521 AA;   57156 MW;   2AC7D22E72D6CAA2 CRC64;

```

Qy	46	PCQLRC-----SSNTPLTDCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPK	101
Db	269	PCP-RCPEPKSCDTPP-PCPR-----CPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPK	320
Qy	102	PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL	161
Db	321	PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVSVL	380
Qy	162	TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT	221
Db	381	TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT	440
Qy	222	CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS	281
Db	441	CLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIF	500
Qy	282	VMHEALHNHYTQKSLSLSPGK	302
Db	501	VMHEALHNRFQKSLSLSPGK	521

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ID      Q8NF17          PRELIMINARY;      PRT;      509 AA.
AC      Q8NF17;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      FLJ00385 protein (Fragment).
GN      FLJ00385.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT      "The nucleotide sequence of a long cDNA clone isolated from human
RT      spleen.";
RL      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AK090464; BAC03445.1; -.
DR      PIR; A45874; A45874.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00407; IGc1; 3.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 2.
FT      NON_TER      1      1
SQ      SEQUENCE      509 AA; 56111 MW; 089498D8076E863C CRC64;

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Qy	46	PCQLRC-----SSNTPLLTQRYCNASVTNSVKGVDKTHTCTPPCPAPELLGGPSVFLFPPK	101
Db	188	PCP-RCPEPKSCDTPP-PCPR-----CPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPK	239
Qy	102	PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL	161
Db	240	PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVSVL	299
Qy	162	TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT	221
Db	300	TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT	359
Qy	222	CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS	281
Db	360	CLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIF	419
Qy	282	VMHEALHNHYTQKSLSLSP	300
Db	420	VMHEALHNRFQKSLSLSP	438

RESULT 8

Q8TC63

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ID      Q8TC63          PRELIMINARY;      PRT;      473 AA.
AC      Q8TC63;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI TaxID=9606;

```


OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wagner B.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98383416; PubMed=9717671;
 RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
 RA Leibold W., Radbruch A.;
 RT "Organization of the equine immunoglobulin heavy chain constant region
 RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
 RL Immunobiology 199:105-119(1998).
 DR EMBL; AJ300675; CAC44624.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 55.8%; Score 917.5; DB 6; Length 337;
 Best Local Similarity 58.7%; Pred. No. 9.6e-79;
 Matches 172; Conservative 42; Mismatches 54; Indels 25; Gaps 3;

QY 12 LLWVPGSTGDVTMLQ MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNS 71
 : : || || : | ::|| : : | : : |
 Db 68 MVTVPAST-----WTSETYICNVVHAASNFKVDKRIEPIPDNHQKVCDS----- 112
 QY 72 VKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 131
 | | ||||| ||||| : || ||||| : ||||| ||||| | : | : |||||
 Db 113 -----KCPKCPAPELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSNQENPDVKFN 164
 QY 132 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 191
 || : ||||| | : | : ||||| : ||||| ||||| : ||||| : ||||| || : ||
 Db 165 WYMDGVEVRTATTRPKKEEQFNSTYRVVSVLRIQHQQDWLSGKEFKCKVNNQALPQPIERTI 224
 QY 192 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTT 249
 : | || : : ||||| | | ||| : : || : ||||| ||| : | : || : ||||| | | ||
 Db 225 TKTGRSQEPQVYVLAPHPDELSKSKVSVTCLVKDFYPPEINIEWQSNQPELETKYSTT 284
 QY 250 PPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
 ||||| : ||||| : || : ||||| | : | ||||| ||||| : : | : |||
 Db 285 QAQQDSGDSYFLYSKLSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK 337

RESULT 10

Q7TMK1

ID Q7TMK1 PRELIMINARY; PRT; 470 AA.
 AC Q7TMK1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC055910; AAH55910.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 52.1%; Score 856; DB 11; Length 470;
Best Local Similarity 61.7%; Pred. No. 1e-72;
Matches 161; Conservative 37; Mismatches 51; Indels 12; Gaps 4;

Qy	52	SSNTPPLTCQRYCN----	ASVTNSVKGVD----	KTHTCP--PCPAPELLGGPSVFLFPPK	101
Db	212	SSTWPSQTV--ICNVAHPASKTELIKRIEPRIPKPSTPPGSSCPPGNILGGPSVFIFPPK	269		
Qy	102	PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL	161		
Db	270	PKDALMISLTPKVTCVVVDVSEDDPDVHVSFVFDNKEVHTAWTQPREAQYNSTFRVVSAL	329		
Qy	162	TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT	221		
		:			
Db	330	PIQHQQDWMRGKEFKCKVNKALPAPIERTISKPKGRAQTPQVYTIPPPREQMSKKKVS	389		
Qy	222	CLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV	281		
Db	390	CLVTNFFSEAI SVEWERNGELEQDYKNTTPILDSGTFLYSLKLTVDTSWLQGEIFTCS	449		

Qy 282 VMHEALHNHYTQKSLSLSPGK 302
 |:|||||:|:|:| |
 Db 450 VVHEALHNHHTQKNLSRSPGK 470

RESULT 11

Q8R3V9

ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
 AC Q8R3V9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC024405; AAH24405.1; -.
 DR PIR; B45837; B45837.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 51.2%; Score 841.5; DB 11; Length 469;
 Best Local Similarity 51.4%; Pred. No. 2.5e-71;
 Matches 164; Conservative 45; Mismatches 71; Indels 39; Gaps 8;

Qy 16 PGSTGDTVMTLQ MAGQCSQNEYF-----DSL LHACIPQLRC----- 51
 ||| : || || | : | | :
 Db 158 PGSAAQTNSMVTLG-CLVKG YFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV 215
 Qy 52 -SSNTPPLTCQRYCNASVTNSVKGVDKTH-----CPP--CPAPELLGGPSVFLFPPKPK 103
 || | | || : | || | | | ||: |||:|||||
 Db 216 PSSTWPSQTVT--CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPPKPK 270
 Qy 104 DTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
 | | | : ||:|||||:| :|||:|:|:| ||| | :|||||:|:|:| || | :
 Db 271 DVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT KPREEQFNSTFRSVSELP I 330
 Qy 164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
 :|||||:|:|:| : | ||||| ||:|: ||||:| :::| :|||:|
 Db 331 MHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCM 390
 Qy 224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVM 283

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      : | : | | | : | | | | | | : | : | : | : | : | | | | : | | : | : | :
Db      391 ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVL 450

Qy      284 HEALHNHYTQKSLSLSPGK 302
      | | | | | : | : | | | | | | |
Db      451 HEGLHNHHTKSLSHSPGK 469

```

RESULT 12

Q99LC4

```

ID      Q99LC4          PRELIMINARY;          PRT;      463 AA.
AC      Q99LC4;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Similar to RIKEN cDNA 1810060009 gene.
GN      IGH-4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC003435; AAH03435.1; -.
DR      PIR; B45837; B45837.
DR      HSSP; P01842; 7FAB.
DR      MGD; MGI:96446; Igh-4.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 1.
SQ      SEQUENCE      463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

```

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Query Match          51.0%;  Score 837.5;  DB 11;  Length 463;
Best Local Similarity 51.1%;  Pred. No. 5.8e-71;
Matches 163;  Conservative 46;  Mismatches 71;  Indels 39;  Gaps 8;

```

```

Qy      16 PGSTGDVTMLQ MAGQCSQNEYF-----DSL LHACIPQLRC----- 51
      | | | : | | | | | | | : | | | |
Db      152 PGSAAQTNSMVTLG-CLVKGYFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV 209

Qy      52 -SSNTPPLTLCQRYCNASVTNSVKGVDKTH-----CPP--CPAPELLGGPSVFLFPPKPK 103
      | | | | | : | | | | | | | | | | | : | | | | | | |
Db      210 PSSTWPSETVT--CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPPKPK 264

Qy      104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
      | | | : | : | | | | | : | : | : | : | | | | | : | | | :
Db      265 DVLITITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELP 324

Qy      164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
      : | | | | | | | : | : | : | | | | | | | | | : | : | : | : |
Db      325 MHQDWLNGKEFKCRVNSAFAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCM 384

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Qy 224 VKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVM 283
 : |:| || |||: |||| ||| | |:|:| |||:|:| || | |: || |:| ||:
 Db 385 ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFIYSKLNQKSNWEAGNTFTCSVL 444

Qy 284 HEALHNHYTQKSLSLSPGK 302
 || ||||:|:| |||| ||||
 Db 445 HEGLHNHHTKSLSHSPGK 463

RESULT 13

Q9R1A4

ID Q9R1A4 PRELIMINARY; PRT; 437 AA.
 AC Q9R1A4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gamma heavy chain of Mab7 (Fragment).
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFV).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF152372; AAD40243.1; -.
 DR PIR; B45837; B45837.
 DR PDB; 1CQK; 11-SEP-99.
 DR PDB; 1I9I; 25-DEC-02.
 DR PDB; 1KCU; 11-MAY-02.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1 1
 FT NON_TER 437 437
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 50.7%; Score 833.5; DB 11; Length 437;
 Best Local Similarity 50.8%; Pred. No. 1.3e-70;
 Matches 162; Conservative 47; Mismatches 71; Indels 39; Gaps 8;

Qy 16 PGSTGDVTMLQ MAGQCSQNEYF-----DSL LHACIPQLRC----- 51
 ||| : || || | :| | |:
 Db 126 PGSAAQTNSMVTLG-CLVKG YFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV 183

Qy 52 --SSNTPPLTCQRYCNASVTNSVKGVDKTH-----CPP--CPAPELLGGPSVFLFPPKPK 103
 || | | : | || | | | ||: |||:|||||

Db 184 PSSTWPSETVT--CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPPKPK 238

Qy 104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
| | | : | | : | | | | | : | : | | | : | : | | | | | : | | | :
Db 239 DVLITITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELP 298

Qy 164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
: | | | | | | | : | : | : | | | | | | | | | | | : | : | : | : | : | :
Db 299 MHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCM 358

Qy 224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV 283
: | : | | | | : | | | | | | | | | | | : | : | : | : | : | : | : | :
Db 359 ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVL 418

Qy 284 HEALHNHYTQKSLSLSPGK 302
| | | | | : | : | : | | | | |
Db 419 HEGLHNHHTTEKNLSHSPGK 437

RESULT 14

Q9D8L4

ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.

DR PIR; S26746; S26746.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Qy	17	GSTGD-----VTMLQMAGQCSQNEY-FDSLHA---CIPCQLRCSNTPP	57
		: : : : : : :	
Db	155	GTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWP	214
Qy	58	---LTCQRYCNASVTVNSVKVD-----KTHTCPPCPAPELLGGPSVFLFPPPKPK	103
		: : : : :	
Db	215	SQTITCNVAHPASSSTKVDDKKIEPRVPITQNPCPLKECPPCAAPDLLGGPSVFIFPPKIK	274
Qy	104	DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT	163
		: : : : : : : : :	
Db	275	DVLMISSLSPMVTCTVVVDVSEDDPDVQISWFVNNEVHTAQTQTHREDYNSTLRVVSALPI	334
Qy	164	LHQDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL	223
		: : : : : : : : : : : : : :	
Db	335	QHQQDWMMSGKEFKCKVNNRALPSPIEKTISKPRGVRAPQVYLPPPAAEEMTKKEFS	394
Qy	224	VKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC	283
		: : : : : : : : : : : : :	
Db	395	ITGFLPAEIAVDWTSGNRTEQNYKNATATVLDSGDFMYSKLRVQKSTWERGSLFACSVV	454
Qy	284	HEALHNHYTQKSLSLSPGK	302
		:	
Db	455	HEGLHNHLTTKTISRSLGK	473

RESULT 15

```

ID     Q99L31          PRELIMINARY;          PRT;    468 AA.
AC     Q99L31;
DT     01-JUN-2001   (TrEMBLrel. 17, Created)
DT     01-JUN-2001   (TrEMBLrel. 17, Last sequence update)
DT     01-OCT-2003   (TrEMBLrel. 25, Last annotation update)
DE     Similar to RIKEN cDNA 1810060O09 gene.
OS     Mus musculus (Mouse).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX     NCBI_TaxID=10090;
RN     [1]
RP     SEQUENCE FROM N.A.
RA     Strausberg R.;
RL     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

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DR EMBL; BC003878; AAH03878.1; -.
 DR PDB; 2AP2; 24-NOV-99.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 49.6%; Score 815.5; DB 11; Length 468;
 Best Local Similarity 54.8%; Pred. No. 7.3e-69;
 Matches 161; Conservative 43; Mismatches 77; Indels 13; Gaps 5;

Qy	22	VTMLQ MAGQCSQNEY-FDSL LHA---CIPCQLRCSSNTPP---LTCQRYCNASVTNSVKG	74
		: : :: : : : :	
Db	175	VTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK	234
Qy	75	VD---KTHTCPP--CPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEV	128
		::	
Db	235	IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPMVT CVVVDVSEDDPDV	294
Qy	129	KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE	188
		: : :	
Db	295	QISW FVNNVEVLTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKALPAPIE	354
Qy	189	KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT	248
		:	
Db	355	RTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN	414
Qy	249	TPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK	302
Db	415	TEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	468

Search completed: April 19, 2004, 13:22:56
 Job time : 45.7407 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:02 ; Search time 12.428 Seconds
(without alignments)
1265.305 Million cell updates/sec

Title: PCT-US03-05147-3
Perfect score: 1643
Sequence: 1 METDTLLLVVLLLVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query			DB ID	Description
		Match	Length			
1	1243	75.7	330	1	GC1_HUMAN	P01857 homo sapien
2	1153	70.2	326	1	GC2_HUMAN	P01859 homo sapien
3	1143.5	69.6	290	1	GC3_HUMAN	P01860 homo sapien
4	1142	69.5	327	1	GC4_HUMAN	P01861 homo sapien
5	934.5	56.9	323	1	GC_RABIT	P01870 oryctolagus
6	903.5	55.0	329	1	GC2_CAVPO	P01862 cavia porce
7	856	52.1	329	1	GC3_MOUSE	P22436 mus musculu
8	849	51.7	333	1	GCB_RAT	P20761 rattus norv
9	845	51.4	398	1	GC3M_MOUSE	P03987 mus musculu
10	827	50.3	326	1	GC1_RAT	P20759 rattus norv
11	826	50.3	329	1	GCC_RAT	P20762 rattus norv
12	825.5	50.2	324	1	GC1_MOUSE	P01868 mus musculu
13	820.5	49.9	393	1	GC1M_MOUSE	P01869 mus musculu
14	819.5	49.9	330	1	GCAA_MOUSE	P01863 mus musculu
15	818.5	49.8	335	1	GCAB_MOUSE	P01864 mus musculu
16	814.5	49.6	399	1	GCAM_MOUSE	P01865 mus musculu
17	796	48.4	322	1	GCA_RAT	P20760 rattus norv

18	789.5	48.1	336	1	GCB_MOUSE	P01866	mus musculu
19	784.5	47.7	405	1	GCBM_MOUSE	P01867	mus musculu
20	362.5	22.1	421	1	EPC_MOUSE	P06336	mus musculu
21	358	21.8	454	1	MUC_HUMAN	P01871	homo sapien
22	357	21.7	455	1	MUC_MOUSE	P01872	mus musculu
23	356	21.7	391	1	MUCB_HUMAN	P04220	homo sapien
24	353	21.5	429	1	EPC_RAT	P01855	rattus norv
25	352	21.4	428	1	EPC_HUMAN	P01854	homo sapien
26	349	21.2	458	1	MUC_RABIT	P03988	oryctolagus
27	347	21.1	476	1	MUCM_MOUSE	P01873	mus musculu
28	339	20.6	479	1	MUCM_RABIT	P04221	oryctolagus
29	332	20.2	450	1	MUC_CANFA	P01874	canis famil
30	332	20.2	454	1	MUC_MESAU	P06337	mesocricetu
31	330.5	20.1	457	1	MUC_SUNMU	P20768	suncus muri
32	310	18.9	438	1	HVC2_HETFR	P23085	heterodontu
33	295.5	18.0	299	1	ALC_RABIT	P01879	oryctolagus
34	294	17.9	438	1	HVCS_HETFR	P23087	heterodontu
35	287.5	17.5	446	1	MUC_CHICK	P01875	gallus gall
36	287	17.5	370	1	HVC1_HETFR	P23084	heterodontu
37	286.5	17.4	184	1	TR17_HUMAN	Q02223	homo sapien
38	285	17.3	461	1	HVCM_HETFR	P23088	heterodontu
39	284.5	17.3	353	1	ALC1_GORGO	P20758	gorilla gor
40	283	17.2	393	1	HVC3_HETFR	P23086	heterodontu
41	280	17.0	353	1	ALC1_HUMAN	P01876	homo sapien
42	271.5	16.5	340	1	ALC2_HUMAN	P01877	homo sapien
43	262.5	16.0	344	1	ALC_MOUSE	P01878	mus musculu
44	251.5	15.3	481	1	MUCM ICTPU	P23735	ictalurus p
45	184.5	11.2	513	1	SHS1_MOUSE	P97797	m protein-t

ALIGNMENTS

RESULT 1

GCl_HUMAN

ID GCl_HUMAN STANDARD; PRT; 330 AA.

AC P01857;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ig gamma-1 chain C region.

GNIGHG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82274238; PubMed=6287432;

RA Ellison J.W., Berson B.J., Hood L.E.;

RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";

RL Nucleic Acids Res. 10:4071-4079(1982).

RN [2]

RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).

RX MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

RA Waxdal M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170(1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181(1970).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC G1M(3) marker and the G1M (non-1) markers.
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of
 CC 35, 116, 198, 269 and 272.
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues

CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.

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 CC -----

DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR PDB; 1AJ7; 12-NOV-97.
 DR PDB; 1D5B; 09-FEB-00.
 DR PDB; 1D5I; 09-FEB-00.
 DR PDB; 1D6V; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1E4K; 06-JUN-01.
 DR PDB; 1FCC; 20-JUL-95.
 DR PDB; 1HZH; 12-JUN-02.
 DR PDB; 1I7Z; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .).
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.


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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      257 PS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALH 316
QY      289 NHYTQKSLSLSPGK 302
                ||||||||||||||||
Db      317 NHYTQKSLSLSPGK 330

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RESULT 2

GC2_HUMAN

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ID      GC2_HUMAN          STANDARD;          PRT;      326 AA.
AC      P01859;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ig gamma-2 chain C region.
GN      IGHG2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE OF 2-326 FROM N.A.
RX      MEDLINE=82197621; PubMed=6804948;
RA      Ellison J.W., Hood L.E.;
RT      "Linkage and sequence homology of two human immunoglobulin gamma
RT      heavy chain constant region genes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN      [2]
RP      SEQUENCE OF 88-115 FROM N.A.
RC      TISSUE=Fetal liver;
RX      MEDLINE=83001943; PubMed=6811139;
RA      Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT      "Structure of human immunoglobulin gamma genes: implications for
RT      evolution of a gene family.";
RL      Cell 29:671-679(1982).
RN      [3]
RP      SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC      TISSUE=Fetal liver;
RX      MEDLINE=84235992; PubMed=6329676;
RA      Krawinkel U., Rabbitts T.H.;
RT      "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT      heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT      genes.";
RL      EMBO J. 1:403-407(1982).
RN      [4]
RP      SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX      MEDLINE=81007873; PubMed=6774012;
RA      Wang A.-C., Tung E., Fudenberg H.H.;
RT      "The primary structure of a human IgG2 heavy chain: genetic,
RT      evolutionary, and functional implications.";
RL      J. Immunol. 125:1048-1054(1980).
RN      [5]
RP      SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX      MEDLINE=80001357; PubMed=113060;
RA      Connell G.E., Parr D.M., Hofmann T.;
RT      "The amino acid sequences of the three heavy chain constant region

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RT domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).

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 CC -----

DR EMBL; J00230; AAB59393.1; -.
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; 1FC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RX MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein Wis.";
 RL Biochemistry 19:4304-4308(1980).
 RN [2]
 RP REVISIONS TO 12-97 (PROTEIN WIS).
 RX MEDLINE=77118561; PubMed=402363;
 RA Michaelsen T.E., Frangione B., Franklin E.C.;
 RT "Primary structure of the 'hinge' region of human IgG3. Probable
 RT quadruplication of a 15-amino acid residue basic unit.";
 RL J. Biol. Chem. 252:883-889(1977).
 RN [3]
 RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
 RX MEDLINE=77021516; PubMed=823945;
 RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
 RT Structure of the Fc fragment of immunoglobulin G3.";
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
 RN [4]
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
 RX MEDLINE=82247835; PubMed=6808505;
 RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
 RA Franklin E.C., Hood L., Buxbaum J.N.;
 RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
 RT gene deletion model.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
 CC -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
 CC interchain disulfide bond at position 7 in addition to the 11
 CC normally present in the hinge region.
 CC -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
 CC -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
 CC Ref.2.
 CC -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
 CC and all of the CH1 region.
 CC -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
 CC of the CH1 region, and part of the hinge compared with normal
 CC gamma-3 heavy chains.
 CC -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
 CC or another gamma chain subclass.
 CC -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
 CC times as long as in other gamma chains and contains three
 CC identical 15-residue segments preceded by a similar 17-residue
 CC segment (12-28).
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 CC -----
 DR EMBL; J00231; AAA52805.1; ALT_SEQ.

DR HSSP; P01857; 1FC1.
 DR Genew; HGNC:5527; IGHG3.
 DR MIM; 147120; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
 KW Pyrrolidone carboxylic acid.
 FT DOMAIN 12 73 HINGE.
 FT DOMAIN 74 183 CH2.
 FT DOMAIN 184 289 CH3.
 FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .).
 FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).
 FT MOD_RES 290 290 REMOVED POST-TRANSLATIONALLY.
 FT VARIANT 126 127 QV -> EB (IN ZUC).
 FT /FTid=VAR_003890.
 FT VARIANT 134 134 P -> L (IN OMM).
 FT /FTid=VAR_003891.
 FT VARIANT 139 139 F -> Y (IN OMM).
 FT /FTid=VAR_003892.
 FT VARIANT 182 182 T -> A (IN OMM).
 FT /FTid=VAR_003893.
 FT VARIANT 227 227 S -> N (IN OMM).
 FT /FTid=VAR_003894.
 FT VARIANT 227 227 MISSING (IN ZUC).
 FT /FTid=VAR_003895.
 FT VARIANT 279 279 F -> Y (IN OMM).
 FT /FTid=VAR_003896.
 SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 69.6%; Score 1143.5; DB 1; Length 290;
 Best Local Similarity 75.6%; Pred. No. 3e-83;
 Matches 220; Conservative 19; Mismatches 37; Indels 15; Gaps 4;

DR EMBL; K01316; AAB59394.1; ALT INIT.

DR PIR; A90933; G4HU.
 DR PDB; 1ADQ; 16-SEP-98.
 DR Genew; HGNC:5528; IGHG4.
 DR MIM; 147130; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 69.5%; Score 1142; DB 1; Length 327;
 Best Local Similarity 85.4%; Pred. No. 4.6e-83;
 Matches 216; Conservative 10; Mismatches 25; Indels 2; Gaps 1;

Qy 52 SSNTPPLTCQRYCNASVTNSVKGVDKTH--TCPPCPAPELLGGPSVFLFPPKPKDTLMIS 109
 | | || | | | : : || |||| |||||
 Db 75 SLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMIS 134
 Qy 110 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 169
 ||||| ||||| |||||:|||||
 Db 135 RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWL 194
 Qy 170 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 229
 ||||| ||| : ||||| :|||:|
 Db 195 NGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYP 254
 Qy 230 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 289
 ||||| :|||:|
 Db 255 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFCSCVMHEALHN 314
 Qy 290 HYTQKSLSLSPGK 302
 ||||| ||
 Db 315 HYTQKSLSLSLGK 327

RESULT 5

GC_RABIT

ID GC_RABIT STANDARD; PRT; 323 AA.

AC P01870;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig gamma chain C region.
 OS *Oryctolagus cuniculus* (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; *Oryctolagus*.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RT F-I haplotype.";
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 RT immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 RT heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 RT immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (In) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 RL Stockholm (1967).
 CC -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
 CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
 CC markers and Ref.5 the E15 marker.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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 CC -----
 DR EMBL; M16426; AAA31289.1; -.
 DR PIR; A91749; GHRB.

Query Match 56.9%; Score 934.5; DB 1; Length 323;
Best Local Similarity 68.0%; Pred. No. 1.1e-66;
Matches 174; Conservative 33; Mismatches 40; Indels 9; Gaps 3;

RESULT 6

GC2_CAVPO

ID GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 55.0%; Score 903.5; DB 1; Length 329;
 Best Local Similarity 65.8%; Pred. No. 3.2e-64;
 Matches 171; Conservative 27; Mismatches 49; Indels 13; Gaps 2;

QY 55 TPPLTCQRYCNASVTNSVKGVDKT-----HTCPPCPAPELLGGPSVFLFPPKPK 103
 | | : : | | : | ||| || | | | | : | | | |
 Db 70 TVPSSQKATCNVAHPASSTKVDKTVEPIRTPZBPBCTCPKCPPPENLGGPSVFIFPPKPK 129
 QY 104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
 | | | | | | | | | | | | | : : | | : | | | | | | | | : | | | :
 Db 130 DTLMISLTPRVTCVVVDVSDPEVEVQFTWFDNKPVGNAETKPRVEQYNTTFRVESVLPI 189
 QY 164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
 | | | | | | : | | | | | | | | | | | | | | | | | : : : | | | |
 Db 190 QHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPSRDELSKSKSVTCL 249
 QY 224 VKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 281
 : | : | : | | | | | | | | | | | : | : | : | | | | | | | | : : | |
 Db 250 IINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSLTVDKSAWDQGTQVYTCS 309
 QY 282 VMHEALHNHYTQKSLSLSPG 301
 | | | | | | | | | | : : | | | |
 Db 310 VMHEALHNHVTQKAISRSPG 329

RESULT 7

GC3_MOUSE

ID GC3_MOUSE STANDARD; PRT; 329 AA.
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;

RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene";
RL EMBO J. 3:2041-2046(1984).

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DR EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 52.1%; Score 856; DB 1; Length 329;
Best Local Similarity 61.7%; Pred. No. 1.8e-60;
Matches 161; Conservative 37; Mismatches 51; Indels 12; Gaps 4;

Qy 52 SSNTPLTCQRYCN-----ASVTNSVKGVD-----KTHTCP--PCPAPELLGGPSVFLFPPK 101
|| | | || || | :| :: | | | :|||||:||||
Db 71 SSTWPSQTV--ICNVAHPASKTELIKRIEPRIPKPSPPGSSCPPGNILGGPSVFIFPPK 128

Qy 102 PKDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 161
||| |||| |::||||||| :||:| :|:| | | | | :||| ||||:|||| |
Db 129 PKDALMISLTPKVTCVVVDVSEDDPDVHVSWSFVDNKEVHTAWTQPREAQYNSTFRVVSAL 188

Qy 162 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 221
: ||||: |||:||||:|||||||:|||| ||: : ||||:| | ::::| :|||
Db 189 PIQHQQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPREQMSKKKSLT 248

Qy 222 CLVKGFFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCS 281
||| |: |:|||| |: | :| |||:||||:||||||| | || :|:|
Db 249 CLVTNFFSEAISVEWERNGELEQDYKNTTPPILSDGTFLYSLKLTVDTDSDLQGEIFTCS 308

Qy 282 VMHEALHNHYTQKSLSLSPGK 302
|:||||||:||||| ||||
Db 309 VVHEALHNHHTQKNLSRSPGK 329

RESULT 8

GCB_RAT

ID GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2B chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 DR PIR; PS0018; PS0018.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 96 IG-LIKE 1.
 FT DOMAIN 124 223 IG-LIKE 2.
 FT DOMAIN 232 328 IG-LIKE 3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 80
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 147 207
 FT DISULFID 253 311
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 51.7%; Score 849; DB 1; Length 333;
 Best Local Similarity 52.6%; Pred. No. 6.5e-60;
 Matches 170; Conservative 42; Mismatches 73; Indels 38; Gaps 6;

Qy 16 PGSTGDVTMLQMGQCSQNEYF-----DSLHACIPCQLR-----CSS 53
 || || | : | || | : | : | : |
 Db 13 PG-CGDTTSSTVTLGCLVKGYFPEPVTVTWNSGALSSDVHT-FPAVLQSGLYTLTSSVTS 70
 Qy 54 NTPP---LTCQRYCNASVTSVKGVDKTH-----TCPPCPAPELLGGPSVFLEP 99
 :| | :|| || | |::: || || |||||:|
 Db 71 STWPSQTVTCNVAHPASSTKVDKVERNRGGIGHKCPTCPTCHKCPVPELLGGPSVFIFP 130
 Qy 100 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 159
 |||| |:|: :||||||| |:|:|:|:|:| ||| |:|:|||||||:|

Db 131 PKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFWNNVEVHTAQTQPREEQYNSTFRVVS 190

QY 160 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 219
 | : ||||:||||:||||:||||||| || |:|||| : | :||: ||

Db 191 ALPIQHQQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPKQVYVMGPPTEQLTEQTVS 250

QY 220 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 279
 |||| || |:|| ||| ||| | ||| | ||:||||||:|||| |:||| |

Db 251 LTCLTSGFLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLNVERSRWDSRAPFV 310

QY 280 CSVMEALHNHYTQKSLSLSPGK 302
 |||:|| ||||: :||:| |||

Db 311 CSVVHEGLHNHHVEKSI SRPPGK 333

RESULT 9

GC3M_MOUSE

ID GC3M_MOUSE STANDARD; PRT; 398 AA.

AC P03987;

DT 23-OCT-1986 (Rel. 02, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-3 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85027161; PubMed=6092053;

RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;

RT "Structural analysis of the murine IgG3 constant region gene.";

RL EMBO J. 3:2041-2046(1984).

RN [2]

RP SEQUENCE OF 328-398 FROM N.A.

RX MEDLINE=84041483; PubMed=6314258;

RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,

RA Wall R.;

RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene

RT segment.";

RL Nucleic Acids Res. 11:6775-6785(1983).

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DR EMBL; J00451; AAB59655.1; -.

DR EMBL; V01526; CAA24767.1; ALT_SEQ.

DR PIR; A02156; G3MSM.

DR HSSP; P01857; 1FC1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 FT TRANSMEM 346 362 POTENTIAL.
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 333 333 E -> G (IN REF. 2).
 FT CONFLICT 342 342 E -> Q (IN REF. 2).
 FT CONFLICT 388 388 P -> F (IN REF. 2).
 SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 51.4%; Score 845; DB 1; Length 398;
 Best Local Similarity 61.4%; Pred. No. 1.7e-59;
 Matches 159; Conservative 37; Mismatches 51; Indels 12; Gaps 4;

Qy 52 SSNTPLTCQRYCN----ASVTSNVKGV-----KTHTCP--PCPAPELLGGPSVFLFPPK 101
 || | | || || :| :: | | | || :|||||:||||
 Db 71 SSTWPSQTV--ICNVAHPASKTELIKRIEPRIPKPKSTPPGSSCPPGNILGGPSVFIFPPK 128
 Qy 102 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 161
 ||| |||| ||:||||||| :||:| :|:| || | | :||| ||||:|||| |
 Db 129 PKDALMISLTPEVTCVVVDVSEDDPDVHVSFVVDNKEVHTAWTQPREAQYNSTFRVVSAL 188
 Qy 162 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 221
 : ||||: |||:||||:|||||||:|||| ||: : ||||:|| |:::| :|||
 Db 189 PIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSLT 248
 Qy 222 CLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS 281
 ||| |: |:|||| ||: | :|| ||:|||||:||||||| | || :|:|
 Db 249 CLVTNFFSEAISVEWERNGELEQDYKNTTPPILDSGDGYFLYSKLTVDTDSDLQGEIFTCS 308
 Qy 282 VMHEALHNHYTQKSLSLSP 300
 |:|||||||:||||:| ||
 Db 309 VVHEALHNHHTQKNLSRSP 327

RESULT 10

GC1_RAT

ID GC1_RAT STANDARD; PRT; 326 AA.

AC P20759;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-1 chain C region.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR; PS0017; PS0017.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 50.3%; Score 827; DB 1; Length 326;
 Best Local Similarity 58.2%; Pred. No. 3.5e-58;
 Matches 152; Conservative 42; Mismatches 51; Indels 16; Gaps 4;

Qy 52 SSNTPPLTCQRYCNASVTNSVKGVDKT-----HTCPPCPAPELLGG---PSVFLFPPK 101
 || | | : | || | | : | ||:||||
 Db 72 SSTWPSQTVT--CNVAHPASSTKVDKKIVPRNCGDCKPC----ICTGSEVSSVFIFPPK 125

 Qy 102 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 161
 || | | : ||:|||||||:| :||| |:|:| ||| |:|:| |||:||||:| || |
 Db 126 PKDVLITITLTPKVTCTVVVDISQDDPEVHFSWFVDDDEVHTAQTRPPEEQFNSTFRSVSEL 185

 Qy 162 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 221
 :|||||||: ::|||:| |:||||||| :|: : | |||: |::|:|:|:|:|
 Db 186 PILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPTEEMTQNEVSIT 245

 Qy 222 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS 281
 |:||||| || |||: |||: ||| ||| :|:|:|:||||| | | :||||| |:|
 Db 246 CMVKGFYPPDIYVEWQMNGQPQENYKNTPTMDTDGSYFLYSLNVKKEKWQQGNFTFTCS 305

 Qy 282 VMHEALHNHYTQKSLSLSPGK 302
 |:|| |||:|:|||| ||||
 Db 306 VLHEGLHNHHTKSLSHSPGK 326

RESULT 11
 GCC_RAT

ID GCC RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).

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DR EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 50.3%; Score 826; DB 1; Length 329;
Best Local Similarity 51.6%; Pred. No. 4.2e-58;
Matches 165; Conservative 51; Mismatches 70; Indels 34; Gaps 7;

Qy 15 VPGSTGDTVTLQMGQCSQNEYF-----DSLHACIPCQLR-----CSSNT 55
||| :| | | | || | :| | | |||
Db 12 VPGSGTSGSLVTLG-CLVKGYFPEPVTWKVNSGALSSGVHT-FPAVLQSGLYTLSSSVT 69


```

RN      [4]
RP      SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX      MEDLINE=78242288; PubMed=98524;
RA      Adetugbo K.;
RT      "Evolution of immunoglobulin subclasses. Primary structure of a
RT      murine myeloma gammal chain.";
RL      J. Biol. Chem. 253:6068-6075(1978).
RN      [5]
RP      DISULFIDE BONDS (MOPC 21).
RX      MEDLINE=73008889; PubMed=5073237;
RA      Svasti J., Milstein C.;
RT      "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL      Biochem. J. 126:837-850(1972).
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC          Name=Secreted;
CC          IsoId=P01868-1; Sequence=Displayed;
CC          Note=May be the major isoform;
CC          Name=Membrane-bound;
CC          IsoId=P01869-1; Sequence=External;
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; V00793; CAA24172.1; -.
DR      EMBL; V00793; CAA24173.1; -.
DR      EMBL; V00793; CAA24174.1; -.
DR      EMBL; V00793; CAA24175.1; -.
DR      EMBL; V00795; CAA24176.1; -.
DR      PIR; A02159; G1MS.
DR      GlycoSuiteDB; P01868; -.
DR      MGD; MGI:96446; Igh-4.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_cl.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 2.
DR      SMART; SM00407; IGcl; 2.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW      Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      1      97      CH1.
FT      DOMAIN      98      110      HINGE.
FT      DOMAIN      111      217      CH2.
FT      DOMAIN      218      324      CH3.
FT      DISULFID      27      82
FT      DISULFID      102      102      INTERCHAIN (WITH A LIGHT CHAIN).
FT      DISULFID      104      104      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      107      107      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      109      109      INTERCHAIN (WITH A HEAVY CHAIN).

```


FT	DISULFID	138	198	
FT	CARBOHYD	174	174	N-LINKED (GLCNAC. . .).
FT				/FTId=CAR_000055.
FT	DISULFID	244	302	
FT	MOD_RES	324	324	REMOVED POST-TRANSLATIONALLY.
FT	CONFLICT	276	276	N -> D (IN REF. 3).
FT	CONFLICT	278	278	N -> D (IN REF. 3).
SO	SEQUENCE	324 AA;	35704 MW;	A338812F3D1F2C93 CRC64;

Query Match 50.2%; Score 825.5; DB 1; Length 324;
Best Local Similarity 51.1%; Pred. No. 4.5e-58;
Matches 162; Conservative 49; Mismatches 71; Indels 35; Gaps 8;

Qy	16	PGSTGDVTFMLQ MAGQCSQNEYF-----DSLLHACIPCQLR-----CSSNTP	56
		: : :	
Db	13	PGSAAQTNSMVTLG-CLVKGYFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV	70
Qy	57	P-----LTCQRYCNASVTN-SVKGVDKTHTCPP--CPAPELLGGPSVFLFPPKPKDT	105
		: : : : : :	
Db	71	PSSPRPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV--SSVFIFPPKPKDV	127
Qy	106	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH	165
		: : : : : : : : : : :	
Db	128	LTITLTPKVTCTVVDISKDDPEVQFSWFVDDEVHTAQTQPREEQFNSTFRSVSELPIMH	187
Qy	166	QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK	225
		: : : : : : : : : : : :	
Db	188	QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMIT	247
Qy	226	GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE	285
		: : : : : : : : : :	
Db	248	DFFPEDITVEWQWNGQPAENYKNTQPIMNITNGSYFVYSKLVNQKSNWEAGNTFTCSVLHE	307
Qy	286	ALHNHYTQKSLSLSPGK	302
		: :	
Db	308	GLHNHHTEKSLSHSPGK	324

RESULT 13

GC1M MOUSE

ID GC1M MOUSE STANDARD; PRT; 393 AA.

AC P01869;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig gamma-1 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=80045036; PubMed=115593;

RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

RA Takahashi N., Mano Y.;

RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";

RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 RT conserved transmembrane sequence and a 28-residue intracellular
 RT domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=Displayed;
 CC Name=Secreted;
 CC IsoId=P01868-1; Sequence=External;
 CC Note=May be the major isoform;
 CC -----
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 CC -----
 DR EMBL; V00793; CAA24172.1; -.
 DR EMBL; V00793; CAA24173.1; -.
 DR EMBL; V00793; CAA24174.1; -.
 DR PIR; B02159; G1MSM.
 DR PDB; 15C8; 23-MAR-99.
 DR PDB; 1AE6; 18-MAR-98.
 DR PDB; 1CL7; 12-JAN-00.
 DR PDB; 1F11; 06-FEB-01.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1KC5; 24-JUL-02.
 DR PDB; 1KCR; 11-MAY-02.
 DR PDB; 25C8; 09-JUL-99.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2A chain C region, A allele.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RT sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Ollo R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE=74175517; PubMed=4831970;
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a
 RT immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462(1972).
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 CC -----
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 CC -----
 DR EMBL; V00798; CAA24178.1; -.
 DR PIR; A02152; G2MSA.
 DR PDB; 1E4W; 12-JUL-01.

DR PDB; 1E4X; 12-JUL-01.
 DR PDB; 1MNU; 06-MAY-99.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 98 IG-LIKE 1.
 FT DOMAIN 121 220 IG-LIKE 2.
 FT DOMAIN 229 325 IG-LIKE 3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 49.9%; Score 819.5; DB 1; Length 330;
 Best Local Similarity 54.8%; Pred. No. 1.4e-57;
 Matches 161; Conservative 43; Mismatches 77; Indels 13; Gaps 5;

QY 22 VTMLQ MAGQCSQNEY-FDSLHA---CIPCQLRCSSNTTP---LTCQRYCNASVTNSVKG 74
 ||: :| | : | ::| : : : :| | :|| || | |
 Db 37 VTILTWN SGLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDK 96
 QY 75 VD----KTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 128
 :: ||| |||| ||||| :||| || |||| :| ||||| :||:|
 Db 97 IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMLSLSPIVTCVVVDVSEDDPDV 156
 QY 129 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 188
 : :|: ||| |::| | ||| ||| | : |||: |||: |||: || |||||
 Db 157 QISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLPAPIE 216
 QY 189 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 248
 : |||| || | |||| ||| : :|| ||: |||: | | || ||| :||: | |||
 Db 217 RTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN 276
 QY 249 TPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
 | ||||| :|: ||| | : | : |||: || |||: | || | :|||
 Db 277 TEPVLDS DGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330

RESULT 15

GCAB_MOUSE

ID GCAB_MOUSE STANDARD; PRT; 335 AA.
 AC P01864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ig gamma-2A chain C region secreted form (B allele).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=82037861; PubMed=6170065;
 RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
 RT "Multiple differences between the nucleic acid sequences of the
 RT IgG2aa and IgG2ab alleles of the mouse.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=82037777; PubMed=6794027;
 RA Dognin M.J., Lauwereys M., Strosberg A.D.;
 RT "Multiple amino acid substitutions between murine gamma 2a heavy
 RT chain Fc regions of Ig1a and Ig1b allotypic forms.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Secreted;
 CC IsoId=P01864-1; Sequence=Displayed;
 CC Note=Probably the major isoform;
 CC Name=Membrane-bound;
 CC IsoId=P01865-1; Sequence=External;
 CC -!- MISCELLANEOUS: The sequence differs from that of the a allele,
 CC from BALB/c mice, at 15% of the positions.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 CC -----
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 CC -----
 DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
 DR PIR; A02153; G2MSAB.
 DR PDB; 1BOG; 23-MAR-99.
 DR PDB; 1HH6; 26-JAN-01.
 DR PDB; 1HH9; 24-JUL-03.
 DR PDB; 1HI6; 08-FEB-01.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
 KW 3D-structure; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 98 IG-LIKE 1.
 FT DOMAIN 126 225 IG-LIKE 2.

FT DOMAIN 234 330 IG-LIKE 3.
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 49.8%; Score 818.5; DB 1; Length 335;
Best Local Similarity 50.8%; Pred. No. 1.7e-57;
Matches 162; Conservative 51; Mismatches 73; Indels 33; Gaps 6;

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Qy      17 GSTGD-----VTMLQ MAGQCSQNEY-FDSLLHA---CIPCQLRCSSNTPP 57
          |:|||          ||:  :|  |  :| :|| :  :  : :||| |
Db      17 GTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWP 76

Qy      58 ---LTCQRYCNASVTNSVKGVD-----KTHTC-----PPCPAPELLGGPSVFLFPPKPK 103
          :||  || |  | ::  : |  ||| ||:|||||||:|||| |
Db      77 SQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPHQVRVPPCAAPDLLGGPSVFIFPPKIK 136

Qy     104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
          | |||| :| ||||| ||| :||:| :|:|: |||| |:|  | |||| |||| | :
Db     137 DVLMI SLSPMVT CVVDVSEDDPDVQISW FVN NVEVHTAQTQTHREDYNSTLRVVSALPI 196

Qy     164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
          ||||:||||:||||:|:||||:||||||| :|  | |||| ||| :|:| | : ||||:
Db     197 QHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLPPPAEEMTKKEFSLTCM 256

Qy     224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVM 283
          : || |:|:| ||:| |||: | ||| | |||||:|:|||| | || |:|:|:|:|:|:|:
Db     257 ITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFACSVV 316

Qy     284 HEALHNHYTQKSLSLSPGK 302
          || |||| | |:| | ||
Db     317 HEVLHNHLTTKTISRSLGK 335
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Search completed: April 19, 2004, 13:21:31
Job time : 13.428 secs